

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 37.2991 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						
No.	Score	Match	Length	DB	ID		Description
1	39	100.0	39	22	AAB80490		PTH2 receptor bind
2	39	100.0	39	23	ABB82202		TIP39 polypeptide
3	39	100.0	39	23	AAE23970		Human TIP39 mature
4	39	100.0	39	24	ABP56764		Human TIP39 protei
5	39	100.0	40	23	AAU73181		Parathyroid hormon
6	38	97.4	38	22	AAB80489		PTH2 receptor bind
7	38	97.4	38	22	AAB80526		PTH2 receptor bind
8	37	94.9	37	22	AAB80488		PTH2 receptor bind
9	37	94.9	37	22	AAB80525		PTH2 receptor bind
10	37	94.9	37	23	ABB82197		TIP39 truncated pe
11	36	92.3	36	22	AAB80487		PTH2 receptor bind
12	36	92.3	36	22	AAB80524		PTH2 receptor bind
13	35	89.7	35	22	AAB80486		PTH2 receptor bind
14	35	89.7	35	22	AAB80523		PTH2 receptor bind
15	35	89.7	35	22	AAB80527		PTH2 receptor bind
16	34	87.2	34	22	AAB80485		PTH2 receptor bind
17	34	87.2	34	22	AAB80522		PTH2 receptor bind
18	34	87.2	34	22	AAB80528		PTH2 receptor bind
19	33	84.6	33	22	AAB80484		PTH2 receptor bind
20	33	84.6	33	22	AAB80521		PTH2 receptor bind
21	33	84.6	33	22	AAB80529		PTH2 receptor bind
22	32	82.1	32	22	AAB80483		PTH2 receptor bind
23	32	82.1	32	22	AAB80520		PTH2 receptor bind
24	32	82.1	32	22	AAB80530		PTH2 receptor bind
25	32	82.1	32	23	ABB82198		TIP39 truncated pe
26	31	79.5	31	22	AAB80482		PTH2 receptor bind
27	31	79.5	31	22	AAB80519		PTH2 receptor bind
28	31	79.5	31	22	AAB80531		PTH2 receptor bind
29	31	79.5	31	23	ABB82196		TIP39 truncated pe
30	30	76.9	30	22	AAB80481		PTH2 receptor bind
31	30	76.9	30	22	AAB80518		PTH2 receptor bind
32	30	76.9	30	22	AAB80532		PTH2 receptor bind
33	30	76.9	30	23	ABB82199		TIP39 truncated pe
34	29	74.4	29	22	AAB80480		PTH2 receptor bind
35	29	74.4	29	22	AAB80517		PTH2 receptor bind
36	29	74.4	29	22	AAB80533		PTH2 receptor bind
37	29	74.4	29	23	ABB82200		TIP39 truncated pe
38	28	71.8	28	22	AAB80479		PTH2 receptor bind
39	28	71.8	28	22	AAB80516		PTH2 receptor bind
40	28	71.8	28	22	AAB80534		PTH2 receptor bind
41	28	71.8	28	23	ABB82201		TIP39 truncated pe
42	28	71.8	37	23	ABB82208		Chimeric PTH1R ago
43	24	61.5	37	23	ABB82209		Chimeric PTH1R ago
44	18	46.2	37	23	ABB82207		Chimeric PTH1R ago
45	6	15.4	28	20	AAU33524		Human p75NTR depen
46	6	15.4	30	23	AAU84792		HCV HepC1a segment
47	6	15.4	30	23	AAU84793		HCV HepC1a segment
48	6	15.4	31	21	AAU77381		HIV-1 group O env
49	6	15.4	31	21	AAU77382		HIV-1 group O env
50	6	15.4	37	17	AAW07210		HIV-1 group O str

51	6	15.4	38	21	AAB14568	HIV-1 isolate CM.A
52	6	15.4	38	22	AAU70740	HIV viral envelope
53	6	15.4	38	22	AAG63895	Amino acid sequenc
54	6	15.4	40	17	AAW07343	Partial sequence o
55	6	15.4	40	17	AAW07344	Partial sequence o
56	6	15.4	40	17	AAW07346	Partial sequence o
57	6	15.4	40	17	AAW07347	Partial sequence o
58	6	15.4	40	17	AAW07352	Partial sequence o
59	5	12.8	28	20	AAV33508	Human p75NTR deriv
60	5	12.8	28	20	AAV33509	Human p75NTR deriv
61	5	12.8	28	20	AAV33510	Human p75NTR deriv
62	5	12.8	28	20	AAV33511	Human p75NTR deriv
63	5	12.8	28	20	AAV33525	Human p75NTR depen
64	5	12.8	28	22	ABG52079	Human liver peptid
65	5	12.8	28	22	ABG52416	Human liver peptid
66	5	12.8	28	22	ABB32003	Peptide #4654 enco
67	5	12.8	28	22	ABB32347	Peptide #4998 enco
68	5	12.8	28	22	ABB37251	Peptide #4757 enco
69	5	12.8	28	22	ABB37608	Peptide #5114 enco
70	5	12.8	28	22	ABB43366	Peptide #10872 enc
71	5	12.8	28	22	ABB22547	Protein #4546 enco
72	5	12.8	28	22	ABB22899	Protein #4898 enco
73	5	12.8	28	22	AAM57958	Human brain expres
74	5	12.8	28	22	AAM58261	Human brain expres
75	5	12.8	28	22	AAM64280	Human brain expres
76	5	12.8	28	22	AAM70383	Human bone marrow
77	5	12.8	28	22	AAM70710	Human bone marrow
78	5	12.8	28	22	AAM77106	Human bone marrow
79	5	12.8	28	22	AAM18225	Peptide #4659 enco
80	5	12.8	28	22	AAM18568	Peptide #5002 enco
81	5	12.8	28	22	AAM30716	Peptide #4753 enco
82	5	12.8	28	22	AAM31026	Peptide #5063 enco
83	5	12.8	28	22	AAM05838	Peptide #4520 enco
84	5	12.8	28	22	AAM06136	Peptide #4818 enco
85	5	12.8	28	23	ABG78097	ITALY, LOR-2, STRI
86	5	12.8	28	23	ABJ01040	Human breast speci
87	5	12.8	28	23	ABG40027	Human peptide enco
88	5	12.8	28	23	ABG40434	Human peptide enco
89	5	12.8	29	19	AAW71425	Peptide having an
90	5	12.8	29	20	AAV01414	Secreted protein e
91	5	12.8	29	21	AAB08357	Amino acid sequenc
92	5	12.8	29	21	AAV95951	Synthetic coiled-c
93	5	12.8	29	21	AAV67645	Peptide #45 for de
94	5	12.8	29	21	AAV67646	Peptide #46 for de
95	5	12.8	29	21	AAV67655	Peptide #55 for de
96	5	12.8	29	21	AAV67656	Peptide #56 for de
97	5	12.8	29	21	AAV67718	Peptide #118 for d
98	5	12.8	29	21	AAV67719	Peptide #119 for d
99	5	12.8	29	21	AAV67728	Peptide #128 for d
100	5	12.8	29	21	AAV67729	Peptide #129 for d
101	5	12.8	29	22	ABG02689	Novel human diagno
102	5	12.8	29	22	AAB81490	Leucine zipper oli
103	5	12.8	30	19	AAW71426	Peptide having an
104	5	12.8	30	21	AAV67636	Peptide #36 for de
105	5	12.8	30	21	AAV67638	Peptide #38 for de
106	5	12.8	30	21	AAV67709	Peptide #109 for d
107	5	12.8	30	21	AAV67711	Peptide #111 for d

108	5	12.8	30	22	ABB50666	Human secreted pro
109	5	12.8	30	22	AAO08695	Human polypeptide
110	5	12.8	30	24	AAE30257	Human LP289 signal
111	5	12.8	31	18	AAW24743	Heel domain of OP-
112	5	12.8	31	19	AAW71427	Peptide having an
113	5	12.8	31	19	AAW80536	Peptide having bet
114	5	12.8	31	19	AAW80538	Peptide having bet
115	5	12.8	31	19	AAW80540	Peptide having bet
116	5	12.8	31	19	AAW80542	Peptide having bet
117	5	12.8	31	19	AAW80544	Peptide having bet
118	5	12.8	31	21	AAAY67665	Peptide #65 for de
119	5	12.8	31	21	AAAY67666	Peptide #66 for de
120	5	12.8	31	21	AAAY67702	Peptide #102 for d
121	5	12.8	31	21	AAAY67703	Peptide #103 for d
122	5	12.8	31	21	AAAY67738	Peptide #138 for d
123	5	12.8	31	21	AAAY67739	Peptide #139 for d
124	5	12.8	31	21	AAAY67775	Peptide #175 for d
125	5	12.8	31	21	AAAY67776	Peptide #176 for d
126	5	12.8	31	23	AAG79849	BMP-7 heel cyclic
127	5	12.8	32	18	AAW36891	Cyclised peptide H
128	5	12.8	32	19	AAW71428	Peptide having an
129	5	12.8	32	19	AAW80537	Peptide having bet
130	5	12.8	32	19	AAW71446	Peptide having an
131	5	12.8	32	19	AAW71439	Peptide having an
132	5	12.8	32	19	AAW71441	Peptide having an
133	5	12.8	32	19	AAW71444	Peptide having an
134	5	12.8	32	21	AAAY67643	Peptide #43 for de
135	5	12.8	32	21	AAAY67644	Peptide #44 for de
136	5	12.8	32	21	AAAY67653	Peptide #53 for de
137	5	12.8	32	21	AAAY67654	Peptide #54 for de
138	5	12.8	32	21	AAAY67716	Peptide #116 for d
139	5	12.8	32	21	AAAY67717	Peptide #117 for d
140	5	12.8	32	21	AAAY67727	Peptide #127 for d
141	5	12.8	32	22	AAU11255	Human osteogenic p
142	5	12.8	32	23	AAG79853	BMP-7 based peptid
143	5	12.8	32	23	ABB76453	BMP-7 antagonist h
144	5	12.8	32	23	ABB76283	Mature human osteo
145	5	12.8	32	24	AAE30262	Human LP319a prote
146	5	12.8	32	24	AAE30266	Human LP319b prote
147	5	12.8	33	11	AAR05848	Reagent of GTP-bin
148	5	12.8	33	11	AAR09313	Reagent of GTP-bin
149	5	12.8	33	19	AAW71421	Peptide having an
150	5	12.8	33	19	AAW71429	Peptide having an
151	5	12.8	33	19	AAW80547	Peptide having bet
152	5	12.8	33	19	AAW71447	Peptide having an
153	5	12.8	33	19	AAW71450	Peptide having an
154	5	12.8	33	19	AAW71451	Peptide having an
155	5	12.8	33	19	AAW71440	Peptide having an
156	5	12.8	33	19	AAW71443	Peptide having an
157	5	12.8	33	19	AAW71445	Peptide having an
158	5	12.8	33	21	AAAY67635	Peptide #35 for de
159	5	12.8	33	21	AAAY67637	Peptide #37 for de
160	5	12.8	33	21	AAAY67708	Peptide #108 for d
161	5	12.8	33	21	AAAY67710	Peptide #110 for d
162	5	12.8	33	22	ABG47640	Human liver peptid
163	5	12.8	33	22	ABB27618	Human peptide #269
164	5	12.8	33	22	ABB32788	Peptide #294 encod

165	5	12.8	33	22	ABB18271	Protein #270 encod
166	5	12.8	33	22	AAM53595	Human brain expres
167	5	12.8	33	22	AAM65975	Human bone marrow
168	5	12.8	33	22	AAM13843	Peptide #277 encod
169	5	12.8	33	22	AAM26250	Peptide #287 encod
170	5	12.8	33	22	AAM01587	Peptide #269 encod
171	5	12.8	33	23	ABG35622	Human peptide enco
172	5	12.8	33	23	ABB76289	Mature human osteo
173	5	12.8	33	24	AAE29925	Human LP289 splice
174	5	12.8	34	19	AAW71422	Peptide having an
175	5	12.8	34	19	AAW71430	Peptide having an
176	5	12.8	34	19	AAW71442	Peptide having an
177	5	12.8	34	19	AAW53038	HIV-1 polypeptide.
178	5	12.8	34	21	AAV67663	Peptide #63 for de
179	5	12.8	34	21	AAV67664	Peptide #64 for de
180	5	12.8	34	21	AAV67700	Peptide #100 for d
181	5	12.8	34	21	AAV67701	Peptide #101 for d
182	5	12.8	34	21	AAV67736	Peptide #136 for d
183	5	12.8	34	21	AAV67737	Peptide #137 for d
184	5	12.8	34	21	AAV67773	Peptide #173 for d
185	5	12.8	34	21	AAV67774	Peptide #174 for d
186	5	12.8	34	21	AAV64930	Human 5' EST relat
187	5	12.8	34	24	ABU70888	Human adipocyte Se
188	5	12.8	35	19	AAW71452	Peptide having an
189	5	12.8	35	19	AAW71453	Peptide having an
190	5	12.8	35	19	AAW71431	Peptide having an
191	5	12.8	35	21	AAB63179	Human secreted pro
192	5	12.8	35	21	AAB29884	Human secreted pro
193	5	12.8	35	21	AAV68726	Amino acid sequenc
194	5	12.8	35	23	ABP42061	Human ovarian anti
195	5	12.8	36	19	AAW71432	Peptide having an
196	5	12.8	36	19	AAW71435	Peptide having an
197	5	12.8	36	19	AAW71436	Peptide having an
198	5	12.8	36	20	AAV30516	Allelic peptide fo
199	5	12.8	36	21	AAV79771	HIV detection rela
200	5	12.8	36	21	AAV55785	HIV (subtype D) pe
201	5	12.8	36	22	AAB62584	Peptide antigen cr
202	5	12.8	36	22	AAB62588	Peptide antigen cr
203	5	12.8	37	19	AAW71433	Peptide having an
204	5	12.8	37	22	ABG49022	Human liver peptid
205	5	12.8	37	22	ABG28237	Novel human diagno
206	5	12.8	37	22	ABB29019	Peptide #1670 enco
207	5	12.8	37	22	ABB34184	Peptide #1690 enco
208	5	12.8	37	22	AAU69966	Human tumour rejec
209	5	12.8	37	22	ABB17893	Human nervous syst
210	5	12.8	37	22	ABB19626	Protein #1625 enco
211	5	12.8	37	22	AAM54977	Human brain expres
212	5	12.8	37	22	AAM67360	Human bone marrow
213	5	12.8	37	22	AAM15192	Peptide #1626 enco
214	5	12.8	37	22	AAM27650	Peptide #1687 enco
215	5	12.8	37	22	AAM02931	Peptide #1613 enco
216	5	12.8	37	23	ABG36993	Human peptide enco
217	5	12.8	37	24	ABP80674	N. gonorrhoeae ami
218	5	12.8	38	19	AAW71434	Peptide having an
219	5	12.8	38	23	ABB82354	Pufferfish urocort
220	5	12.8	39	20	AAV12400	Human 5' EST secre
221	5	12.8	39	22	ABG56473	Human liver peptid

222	5	12.8	39	22	ABB41032	Peptide #8538 enco
223	5	12.8	39	22	AAM61887	Human brain expres
224	5	12.8	39	22	AAM74689	Human bone marrow
225	5	12.8	39	22	AAM34805	Peptide #8842 enco
226	5	12.8	39	23	ABJ10284	Human lung specifi
227	5	12.8	39	23	ABG44502	Human peptide enco
228	5	12.8	40	20	AA111858	Human 5' EST secre
229	5	12.8	40	22	AA011965	Human polypeptide
230	5	12.8	40	22	AAB45730	Human 7TM clone H7
231	4	10.3	28	9	AAP80199	Sequence of vasoac
232	4	10.3	28	12	AAR10938	N-terminal sequenc
233	4	10.3	28	12	AAR11313	N-terminal of deac
234	4	10.3	28	12	AAR14755	Modified expressio
235	4	10.3	28	13	AAR27568	Pel B leader plus
236	4	10.3	28	13	AAR27570	Pel B leader to fu
237	4	10.3	28	14	AAR54342	RAE 22.E. Ambrosi
238	4	10.3	28	14	AAR54407	AMB 1-6.1. Ambros
239	4	10.3	28	14	AAR40315	VIP analogue (37).
240	4	10.3	28	15	AAR53100	Bronchodilator pep
241	4	10.3	28	15	AAR53102	Bronchodilator pep
242	4	10.3	28	15	AAR53106	Bronchodilator pep
243	4	10.3	28	16	AAR85555	Deamidating antibo
244	4	10.3	28	16	AAR72982	Calmodulin-binding
245	4	10.3	28	16	AAR64328	HSV L/ST ORF2. He
246	4	10.3	28	16	AAR70261	Partial IGF-I fusi
247	4	10.3	28	17	AAW16418	Human growth facto
248	4	10.3	28	17	AAW16419	Human growth facto
249	4	10.3	28	17	AAW16425	Human growth facto
250	4	10.3	28	17	AAW16441	Human growth facto
251	4	10.3	28	17	AAW02429	RAE 22.E comprisin
252	4	10.3	28	17	AAW02393	AMB 1-6.1 comprisi
253	4	10.3	28	19	AA121363	Human HUPF-I mutan
254	4	10.3	28	19	AA121018	Human glial fibril
255	4	10.3	28	19	AAW74926	Human secreted pro
256	4	10.3	28	19	AAW39968	Peptide effecting
257	4	10.3	28	19	AAW39979	Peptide effecting
258	4	10.3	28	20	AA133513	Human p75NTR depen
259	4	10.3	28	20	AA139255	G-protein coupled
260	4	10.3	28	20	AA130517	Allelic peptide fo
261	4	10.3	28	20	AA140049	Peptide sequence d
262	4	10.3	28	20	AA140084	Peptide sequence d
263	4	10.3	28	20	AA136409	Fragment of human
264	4	10.3	28	20	AA107850	Human secreted pro
265	4	10.3	28	20	AAW81051	Signal peptide-cyt
266	4	10.3	28	20	AAW52786	Human growth hormo
267	4	10.3	28	20	AAW52770	Human growth hormo
268	4	10.3	28	20	AAW52763	Human growth hormo
269	4	10.3	28	20	AAW52764	Human growth hormo
270	4	10.3	28	21	AAB29919	Human secreted pro
271	4	10.3	28	21	AAB29920	Human secreted pro
272	4	10.3	28	21	AAB22003	Human V gene Vbeta
273	4	10.3	28	21	AA171038	Streptococcus pyog
274	4	10.3	28	21	AA195080	Leader sequence us
275	4	10.3	28	21	AA198189	Leader sequence us
276	4	10.3	28	21	AA179772	HIV detection rela
277	4	10.3	28	21	AA179811	HIV infection dete
278	4	10.3	28	21	AA151395	Human VDCCalpha1 p

279	4	10.3	28	21	AAAY54385	Amino acid sequenc
280	4	10.3	28	21	AAAY54393	Amino acid sequenc
281	4	10.3	28	21	AAAY54401	Amino acid sequenc
282	4	10.3	28	22	ABG47988	Human liver peptid
283	4	10.3	28	22	ABG52148	Human liver peptid
284	4	10.3	28	22	ABG54715	Human liver peptid
285	4	10.3	28	22	ABG56266	Human liver peptid
286	4	10.3	28	22	ABG58974	Human liver peptid
287	4	10.3	28	22	ABG03282	Novel human diagno
288	4	10.3	28	22	ABB27966	Human peptide #617
289	4	10.3	28	22	ABB32080	Peptide #4731 enco
290	4	10.3	28	22	ABB33138	Peptide #644 encod
291	4	10.3	28	22	ABB37334	Peptide #4840 enco
292	4	10.3	28	22	ABB39655	Peptide #7161 enco
293	4	10.3	28	22	ABB40823	Peptide #8329 enco
294	4	10.3	28	22	ABB43598	Peptide #11104 enc
295	4	10.3	28	22	ABB18603	Protein #602 encod
296	4	10.3	28	22	ABB22621	Protein #4620 enco
297	4	10.3	28	22	ABB24331	Protein #6330 enco
298	4	10.3	28	22	ABB25002	Protein #7001 enco
299	4	10.3	28	22	ABB26552	Protein #8551 enco
300	4	10.3	28	22	AAM53934	Human brain expres
301	4	10.3	28	22	AAM58025	Human brain expres
302	4	10.3	28	22	AAM60367	Human brain expres
303	4	10.3	28	22	AAM61681	Human brain expres
304	4	10.3	28	22	AAM64537	Human brain expres
305	4	10.3	28	22	AAM66322	Human bone marrow
306	4	10.3	28	22	AAM70462	Human bone marrow
307	4	10.3	28	22	AAM73004	Human bone marrow
308	4	10.3	28	22	AAM74474	Human bone marrow
309	4	10.3	28	22	AAM77342	Human bone marrow
310	4	10.3	28	22	AAM89401	Human immune/haema
311	4	10.3	28	22	AAM14191	Peptide #625 encod
312	4	10.3	28	22	AAM18298	Peptide #4732 enco
313	4	10.3	28	22	AAM19801	Peptide #6235 enco
314	4	10.3	28	22	AAM20325	Peptide #6759 enco
315	4	10.3	28	22	AAM21265	Peptide #7699 enco
316	4	10.3	28	22	AAM26601	Peptide #638 encod
317	4	10.3	28	22	AAM30784	Peptide #4821 enco
318	4	10.3	28	22	AAM33228	Peptide #7265 enco
319	4	10.3	28	22	AAM34589	Peptide #8626 enco
320	4	10.3	28	22	AAM37492	Peptide #11529 enc
321	4	10.3	28	22	AAM01927	Peptide #609 encod
322	4	10.3	28	22	AAM05907	Peptide #4589 enco
323	4	10.3	28	22	AAB62595	Peptide antigen cr
324	4	10.3	28	22	AAE01634	Human gene 5 encod
325	4	10.3	28	22	AAB74345	Peptide SAF-p2A.
326	4	10.3	28	22	AAB74346	Peptide SAF-p2B.
327	4	10.3	28	22	AAB74347	Peptide SAF-p2C.
328	4	10.3	28	22	AAB74348	Peptide SAF-p2D.
329	4	10.3	28	22	AAB74349	Peptide SAF-p2E.
330	4	10.3	28	22	AAB74352	Peptide SAF-p2. U
331	4	10.3	28	22	AAB74356	Peptide used to fo
332	4	10.3	28	22	AAB68568	Peptide #2. Unide
333	4	10.3	28	22	AAB50218	Membrane disruptiv
334	4	10.3	28	22	AAB50230	Membrane disruptiv
335	4	10.3	28	23	ABG95380	Human novel secret

336	4	10.3	28	23	ABG93993	Human vasoactive i
337	4	10.3	28	23	ABG94089	Human vasoactive i
338	4	10.3	28	23	ABG78098	ITALY, LOR-2, STRI
339	4	10.3	28	23	AAE25431	Human Nod2 protein
340	4	10.3	28	23	ABJ04750	Nod2 leucine-rich
341	4	10.3	28	23	ABJ04781	Nod2 exon 11 pepti
342	4	10.3	28	23	AAO22121	Human CARD related
343	4	10.3	28	23	AAE23916	Human TCR Vbeta1 p
344	4	10.3	28	23	ABG35970	Human peptide enco
345	4	10.3	28	23	ABG40100	Human peptide enco
346	4	10.3	28	23	ABG42843	Human peptide enco
347	4	10.3	28	23	ABG44356	Human peptide enco
348	4	10.3	28	23	ABG46357	Human peptide enco
349	4	10.3	28	23	AAU91197	Human E1-E2 ATPase
350	4	10.3	28	23	AAU83142	Novel secreted pro
351	4	10.3	28	23	ABB04529	Hepatitis C capsid
352	4	10.3	28	23	ABB04559	Hepatitis C capsid
353	4	10.3	28	24	ABU56283	Human CARD-4L, Leu
354	4	10.3	28	24	ABP57664	Human CNI-00713 OR
355	4	10.3	29	8	AAP71212	Sequence of peptid
356	4	10.3	29	8	AAP71213	Sequence of peptid
357	4	10.3	29	8	AAP71214	Sequence of peptid
358	4	10.3	29	8	AAP71215	Sequence of peptid
359	4	10.3	29	8	AAP71216	Sequence of peptid
360	4	10.3	29	8	AAP71217	Sequence of peptid
361	4	10.3	29	8	AAP71218	Sequence of peptid
362	4	10.3	29	13	AAR28772	GHRF analogue pept
363	4	10.3	29	14	AAR44425	Mutant alpha-amyla
364	4	10.3	29	14	AAR44426	Mutant alpha-amyla
365	4	10.3	29	14	AAR44427	Mutant alpha-amyla
366	4	10.3	29	14	AAR44428	Mutant alpha-amyla
367	4	10.3	29	16	AAR74847	CDR3 sequence of T
368	4	10.3	29	16	AAR74848	CDR3 sequence of T
369	4	10.3	29	16	AAR74834	CDR3 sequence of T
370	4	10.3	29	17	AAW07235	HIV-1 group O stra
371	4	10.3	29	17	AAR92880	Mycobacterium 45 k
372	4	10.3	29	17	AAR89960	Synthetic human er
373	4	10.3	29	17	AAR93929	Integrin subunit b
374	4	10.3	29	18	AAW33829	CDR3 sequence of T
375	4	10.3	29	18	AAW33842	CDR3 sequence of T
376	4	10.3	29	18	AAW33843	CDR3 sequence of T
377	4	10.3	29	19	AAW75582	M. tuberculosis 45
378	4	10.3	29	19	AAW40023	Peptide effecting
379	4	10.3	29	20	AAAY11909	Human 5' EST secre
380	4	10.3	29	20	AAAY10849	Amino acid sequenc
381	4	10.3	29	21	AAB39209	Human secreted pro
382	4	10.3	29	21	AAB40181	Human secreted pro
383	4	10.3	29	21	AAB15448	TCR beta V-N-J reg
384	4	10.3	29	21	AAB12060	Ad7 crl peptide.
385	4	10.3	29	21	AAB12062	EA7 crl peptide.
386	4	10.3	29	21	AAB22011	Human V gene Vbeta
387	4	10.3	29	21	AAAY70894	N-terminal portion
388	4	10.3	29	21	AAAY70917	N-terminal portion
389	4	10.3	29	21	AAAY53253	Human type enzyme
390	4	10.3	29	21	AAAY79831	HIV infection dete
391	4	10.3	29	21	AAAY86444	Human gene 42-enco
392	4	10.3	29	21	AAAY54386	Amino acid sequenc

393	4	10.3	29	21	AAAY54394	Amino acid sequenc
394	4	10.3	29	21	AAAY54402	Amino acid sequenc
395	4	10.3	29	21	AAAY67657	Peptide #57 for de
396	4	10.3	29	21	AAAY67658	Peptide #58 for de
397	4	10.3	29	21	AAAY67659	Peptide #59 for de
398	4	10.3	29	21	AAAY67660	Peptide #60 for de
399	4	10.3	29	21	AAAY67730	Peptide #130 for d
400	4	10.3	29	21	AAAY67731	Peptide #131 for d
401	4	10.3	29	21	AAAY67732	Peptide #132 for d
402	4	10.3	29	21	AAAY67733	Peptide #133 for d
403	4	10.3	29	22	ABG53190	Human liver peptid
404	4	10.3	29	22	ABG54049	Human liver peptid
405	4	10.3	29	22	ABG55455	Human liver peptid
406	4	10.3	29	22	ABG55564	Human liver peptid
407	4	10.3	29	22	ABG55595	Human liver peptid
408	4	10.3	29	22	ABG57326	Human liver peptid
409	4	10.3	29	22	ABG00774	Novel human diagno
410	4	10.3	29	22	ABB38357	Peptide #5863 enco
411	4	10.3	29	22	ABB39125	Peptide #6631 enco
412	4	10.3	29	22	ABB40308	Peptide #7814 enco
413	4	10.3	29	22	ABB40334	Peptide #7840 enco
414	4	10.3	29	22	ABB41890	Peptide #9396 enco
415	4	10.3	29	22	ABB23534	Protein #5533 enco
416	4	10.3	29	22	ABB24022	Protein #6021 enco
417	4	10.3	29	22	ABB24711	Protein #6710 enco
418	4	10.3	29	22	AAM58968	Human brain expres
419	4	10.3	29	22	AAM59778	Human brain expres
420	4	10.3	29	22	AAM61106	Human brain expres
421	4	10.3	29	22	AAM61135	Human brain expres
422	4	10.3	29	22	AAM62766	Human brain expres
423	4	10.3	29	22	AAM71495	Human bone marrow
424	4	10.3	29	22	AAM72362	Human bone marrow
425	4	10.3	29	22	AAM73715	Human bone marrow
426	4	10.3	29	22	AAM73814	Human bone marrow
427	4	10.3	29	22	AAM73845	Human bone marrow
428	4	10.3	29	22	AAM75584	Human bone marrow
429	4	10.3	29	22	AAM19148	Peptide #5582 enco
430	4	10.3	29	22	AAM19557	Peptide #5991 enco
431	4	10.3	29	22	AAM20110	Peptide #6544 enco
432	4	10.3	29	22	AAM31796	Peptide #5833 enco
433	4	10.3	29	22	AAM32618	Peptide #6655 enco
434	4	10.3	29	22	AAM33901	Peptide #7938 enco
435	4	10.3	29	22	AAM34000	Peptide #8037 enco
436	4	10.3	29	22	AAM34030	Peptide #8067 enco
437	4	10.3	29	22	AAM35689	Peptide #9726 enco
438	4	10.3	29	22	AAG76872	Human colon cancer
439	4	10.3	29	22	AAE03839	Human gene 22 enco
440	4	10.3	29	22	AAE03869	Human gene 22 enco
441	4	10.3	29	22	AAB62697	ABCl protein exter
442	4	10.3	29	22	AAB81491	Leucine zipper oli
443	4	10.3	29	23	ABG95603	Human novel secret
444	4	10.3	29	23	AAE26389	Human GPR10 protei
445	4	10.3	29	23	ABP62086	Human secreted pro
446	4	10.3	29	23	AAU99914	Human 47476 EF-han
447	4	10.3	29	23	ABG67083	Streptavidin-bindi
448	4	10.3	29	23	AAE23924	Human TCR Vbeta7 p
449	4	10.3	29	23	ABG64549	Human albumin fusi

450	4	10.3	29	23	ABG64550	Human albumin fusi
451	4	10.3	29	23	ABG41308	Human peptide enco
452	4	10.3	29	23	ABG42178	Human peptide enco
453	4	10.3	29	23	ABG43592	Human peptide enco
454	4	10.3	29	23	ABG43703	Human peptide enco
455	4	10.3	29	23	AAU91212	Human E1-E2 ATPase
456	4	10.3	29	23	AAE16229	Human betaig-h3 fi
457	4	10.3	29	23	ABB04551	Hepatitis C capsid
458	4	10.3	29	24	ABG74421	M. tuberculosis ex
459	4	10.3	29	24	ABU57605	Synthetic peptide
460	4	10.3	29	24	ABP60610	Rat insulin recept
461	4	10.3	29	24	ABJ18866	Human Bcl-XL-bind
462	4	10.3	29	24	ABJ18879	Human Bcl-XL-bind
463	4	10.3	30	2	AAP10040	Sequence encoded b
464	4	10.3	30	4	AAP30309	Sequence of peptid
465	4	10.3	30	9	AAP82087	Polypeptide pN4(30
466	4	10.3	30	9	AAP81553	Human insulin acce
467	4	10.3	30	10	AAP90125	Pectate lyase sign
468	4	10.3	30	13	AAR24421	Sequence of T help
469	4	10.3	30	13	AAR25214	Immunosuppressive
470	4	10.3	30	15	AAR47980	L. brevis DSM20556
471	4	10.3	30	15	AAR37123	Decarbamylase N-te
472	4	10.3	30	16	AAR74833	CDR3 sequence of T
473	4	10.3	30	16	AAR78750	PelB leader peptid
474	4	10.3	30	16	AAR75651	Human placenta der
475	4	10.3	30	16	AAR85676	45 kD M.tuberculos
476	4	10.3	30	17	AAR89965	Synthetic human er
477	4	10.3	30	18	AAW34148	Analogue #4 of HTL
478	4	10.3	30	18	AAW33828	CDR3 sequence of T
479	4	10.3	30	18	AAW22398	Human urocortin pe
480	4	10.3	30	18	AAW16345	Erwinia carotovora
481	4	10.3	30	18	AAW14016	N-terminus of Stap
482	4	10.3	30	18	AAW10244	Pel B signal seque
483	4	10.3	30	18	AAW18194	N-terminal sequenc
484	4	10.3	30	19	AAW74852	Human secreted pro
485	4	10.3	30	19	AAW47516	Erwinia carotovora
486	4	10.3	30	19	AAW47523	Erwinia carotovora
487	4	10.3	30	19	AAW41075	Erwinia carotovora
488	4	10.3	30	20	AAY33140	Rabbit liver carbo
489	4	10.3	30	20	AAY17970	Peptide Seq ID No:
490	4	10.3	30	20	AAY13409	Peptide from HSV1
491	4	10.3	30	20	AAY07214	Peptide transfecti
492	4	10.3	30	20	AAW89542	A pectate lyase pe
493	4	10.3	30	21	AAB62906	Human MGST-II alte
494	4	10.3	30	21	AAB36465	Human plakophilin
495	4	10.3	30	21	AAB34508	Human secreted pro
496	4	10.3	30	21	AAB39081	Human secreted pro
497	4	10.3	30	21	AAB45036	Human secreted pro
498	4	10.3	30	21	AAB15438	TCR beta V-N-J reg
499	4	10.3	30	21	AAB15481	TCR beta V-N-J reg
500	4	10.3	30	21	AAG35977	Arabidopsis thalia
501	4	10.3	30	21	AAY85074	Immunogenic peptid
502	4	10.3	30	21	AAY79837	HIV infection dete
503	4	10.3	30	21	AAY54387	Amino acid sequenc
504	4	10.3	30	21	AAY54395	Amino acid sequenc
505	4	10.3	30	21	AAY54403	Amino acid sequenc
506	4	10.3	30	21	AAY67639	Peptide #39 for de

507	4	10.3	30	21	AAAY67640	Peptide #40 for de
508	4	10.3	30	21	AAAY67641	Peptide #41 for de
509	4	10.3	30	21	AAAY67642	Peptide #42 for de
510	4	10.3	30	21	AAAY67647	Peptide #47 for de
511	4	10.3	30	21	AAAY67648	Peptide #48 for de
512	4	10.3	30	21	AAAY67649	Peptide #49 for de
513	4	10.3	30	21	AAAY67650	Peptide #50 for de
514	4	10.3	30	21	AAAY67713	Peptide #113 for d
515	4	10.3	30	21	AAAY67714	Peptide #114 for d
516	4	10.3	30	21	AAAY67715	Peptide #115 for d
517	4	10.3	30	21	AAAY67720	Peptide #120 for d
518	4	10.3	30	21	AAAY67721	Peptide #121 for d
519	4	10.3	30	21	AAAY67722	Peptide #122 for d
520	4	10.3	30	21	AAAY67723	Peptide #123 for d
521	4	10.3	30	21	AAAY67726	Peptide #126 for d
522	4	10.3	30	22	ABG53218	Human liver peptid
523	4	10.3	30	22	ABG57529	Human liver peptid
524	4	10.3	30	22	ABG00496	Novel human diagno
525	4	10.3	30	22	ABG02839	Novel human diagno
526	4	10.3	30	22	ABG07265	Novel human diagno
527	4	10.3	30	22	ABG11764	Novel human diagno
528	4	10.3	30	22	ABB38389	Peptide #5895 enco
529	4	10.3	30	22	ABB42098	Peptide #9604 enco
530	4	10.3	30	22	ABB23567	Protein #5566 enco
531	4	10.3	30	22	AAM58998	Human brain expres
532	4	10.3	30	22	AAM62978	Human brain expres
533	4	10.3	30	22	AAM71526	Human bone marrow
534	4	10.3	30	22	AAM75791	Human bone marrow
535	4	10.3	30	22	AAM88420	Human immune/haema
536	4	10.3	30	22	AAM19180	Peptide #5614 enco
537	4	10.3	30	22	AAM31826	Peptide #5863 enco
538	4	10.3	30	22	AAM35901	Peptide #9938 enco
539	4	10.3	30	22	AAB98097	Erwinia caratovora
540	4	10.3	30	22	AAB92014	Galanin peptide SE
541	4	10.3	30	23	ABP68891	Marine snail beta-
542	4	10.3	30	23	ABG95303	Human novel secret
543	4	10.3	30	23	AAU97984	Synthetic erythrop
544	4	10.3	30	23	AAU97991	Synthetic erythrop
545	4	10.3	30	23	AAU97995	Synthetic erythrop
546	4	10.3	30	23	ABG41339	Human peptide enco
547	4	10.3	30	23	ABP41453	Human ovarian anti
548	4	10.3	30	23	AAO17273	A thaliana recepto
549	4	10.3	30	23	AAU84532	HIV VPU segment 3.
550	4	10.3	30	23	AAU84533	HIV VPU segment 4.
551	4	10.3	30	23	AAU84617	HCV HepC1a segment
552	4	10.3	30	23	AAU84647	HCV HepC1a segment
553	4	10.3	30	23	AAU84665	HCV HepC1a segment
554	4	10.3	30	23	AAU84666	HCV HepC1a segment
555	4	10.3	30	23	AAU84708	HCV HepC1a segment
556	4	10.3	30	23	AAU84709	HCV HepC1a segment
557	4	10.3	30	23	AAU84797	HCV HepC1a segment
558	4	10.3	30	23	AAU84860	Human gp100 segmen
559	4	10.3	30	23	AAU84861	Human gp100 segmen
560	4	10.3	30	23	AAU84997	Human MUC1R segmen
561	4	10.3	30	23	AAU85000	Human MUC1R segmen
562	4	10.3	30	23	AAU85001	Human MUC1R segmen
563	4	10.3	30	23	AAU85067	Human PRAME segmen

564	4	10.3	30	24	ABP59412	Self-assembling tr
565	4	10.3	30	24	ABP59413	Self-assembling tr
566	4	10.3	30	24	ABR01204	Human gene 258-enc
567	4	10.3	30	24	ABU56346	M. tuberculosis ex
568	4	10.3	30	24	ABJ19714	Human secreted pro
569	4	10.3	30	24	ABP99721	Human secreted pro
570	4	10.3	30	24	ABR00921	Bioactive syntheti
571	4	10.3	30	24	ABP55255	Human histamine H2
572	4	10.3	31	8	AAP70904	Herpes simplex vir
573	4	10.3	31	11	AAR07739	Lytic peptide with
574	4	10.3	31	14	AAR42700	p19 of nef peptide
575	4	10.3	31	15	AAR54745	pRAS117 sequence b
576	4	10.3	31	16	AAR74849	CDR3 sequence of T
577	4	10.3	31	16	AAR74850	CDR3 sequence of T
578	4	10.3	31	16	AAR74851	CDR3 sequence of T
579	4	10.3	31	17	AAW03903	Glucagon like pept
580	4	10.3	31	17	AAW03971	VDJ joint protein,
581	4	10.3	31	18	AAW41134	VH251 DK1 J2 gamma
582	4	10.3	31	18	AAW33846	CDR3 sequence of T
583	4	10.3	31	18	AAW33844	CDR3 sequence of T
584	4	10.3	31	18	AAW33845	CDR3 sequence of T
585	4	10.3	31	18	AAW17085	Foot and mouth dis
586	4	10.3	31	18	AAW12463	Control peptide si
587	4	10.3	31	18	AAW19976	Fibronectin fragme
588	4	10.3	31	19	AAW72581	Zea mays soluble s
589	4	10.3	31	19	AAW40009	Peptide effecting
590	4	10.3	31	19	AAW39981	Peptide effecting
591	4	10.3	31	19	AAW39787	Synthetic peptide
592	4	10.3	31	20	AAAY40402	Amino acid sequenc
593	4	10.3	31	20	AAAY36384	Fragment of human
594	4	10.3	31	20	AAAY07948	Human secreted pro
595	4	10.3	31	20	AAAY12905	Human 5' EST secre
596	4	10.3	31	20	AAAY12350	Human 5' EST secre
597	4	10.3	31	20	AAAY11996	Human 5' EST secre
598	4	10.3	31	20	AAAY11630	Human 5' EST secre
599	4	10.3	31	20	AAAY10862	Amino acid sequenc
600	4	10.3	31	20	AAW88668	Secreted protein e
601	4	10.3	31	20	AAW73494	Cellobiose phospho
602	4	10.3	31	20	AAW82987	Human fibronectin
603	4	10.3	31	21	AAB28325	Human secreted pep
604	4	10.3	31	21	AAB27918	Human secreted pro
605	4	10.3	31	21	AAB39011	Human secreted pep
606	4	10.3	31	21	AAB39082	Human secreted pro
607	4	10.3	31	21	AAB15490	TCR beta V-N-J reg
608	4	10.3	31	21	AAB15491	TCR beta V-N-J reg
609	4	10.3	31	21	AAB15704	Mitochondrial matr
610	4	10.3	31	21	AAB22012	Human V gene Vbeta
611	4	10.3	31	21	AAB22037	Peptide #3 contain
612	4	10.3	31	21	AAB22041	Molecular velcro p
613	4	10.3	31	21	AAB22043	Peptide #2 contain
614	4	10.3	31	21	AAB22045	PKA peptide #1. U
615	4	10.3	31	21	AAB22835	Mitochondrial matr
616	4	10.3	31	21	AAG21998	Arabidopsis thalia
617	4	10.3	31	21	AAAY70895	N-terminal portion
618	4	10.3	31	21	AAAY70918	N-terminal portion
619	4	10.3	31	21	AAAY54388	Amino acid sequenc
620	4	10.3	31	21	AAAY54396	Amino acid sequenc

621	4	10.3	31	21	AAAY54404	Amino acid sequenc
622	4	10.3	31	21	AAAY67667	Peptide #67 for de
623	4	10.3	31	21	AAAY67668	Peptide #68 for de
624	4	10.3	31	21	AAAY67669	Peptide #69 for de
625	4	10.3	31	21	AAAY67670	Peptide #70 for de
626	4	10.3	31	21	AAAY67704	Peptide #104 for d
627	4	10.3	31	21	AAAY67705	Peptide #105 for d
628	4	10.3	31	21	AAAY67706	Peptide #106 for d
629	4	10.3	31	21	AAAY67707	Peptide #107 for d
630	4	10.3	31	21	AAAY67740	Peptide #140 for d
631	4	10.3	31	21	AAAY67741	Peptide #141 for d
632	4	10.3	31	21	AAAY67742	Peptide #142 for d
633	4	10.3	31	21	AAAY67743	Peptide #143 for d
634	4	10.3	31	21	AAAY67778	Peptide #178 for d
635	4	10.3	31	21	AAAY67779	Peptide #179 for d
636	4	10.3	31	21	AAAY67780	Peptide #180 for d
637	4	10.3	31	21	AAAY55087	C. trachomatis maj
638	4	10.3	31	21	AAAY65000	Human 5' EST relat
639	4	10.3	31	22	ABG49117	Human liver peptid
640	4	10.3	31	22	ABG50769	Human liver peptid
641	4	10.3	31	22	ABG53284	Human liver peptid
642	4	10.3	31	22	ABG53386	Human liver peptid
643	4	10.3	31	22	ABG55017	Human liver peptid
644	4	10.3	31	22	ABG26988	Novel human diagno
645	4	10.3	31	22	ABB29115	Peptide #1766 enco
646	4	10.3	31	22	ABB30734	Peptide #3385 enco
647	4	10.3	31	22	ABB34276	Peptide #1782 enco
648	4	10.3	31	22	ABB35909	Peptide #3415 enco
649	4	10.3	31	22	ABB38458	Peptide #5964 enco
650	4	10.3	31	22	ABB38543	Peptide #6049 enco
651	4	10.3	31	22	ABB39891	Peptide #7397 enco
652	4	10.3	31	22	ABB50435	Human secreted pro
653	4	10.3	31	22	ABB19708	Protein #1707 enco
654	4	10.3	31	22	ABB21319	Protein #3318 enco
655	4	10.3	31	22	ABB23622	Protein #5621 enco
656	4	10.3	31	22	AAB35489	Internalising pept
657	4	10.3	31	22	AAM55069	Human brain expres
658	4	10.3	31	22	AAM56714	Human brain expres
659	4	10.3	31	22	AAM59069	Human brain expres
660	4	10.3	31	22	AAM59166	Human brain expres
661	4	10.3	31	22	AAM60631	Human brain expres
662	4	10.3	31	22	AAM67462	Human bone marrow
663	4	10.3	31	22	AAM69089	Human bone marrow
664	4	10.3	31	22	AAM71602	Human bone marrow
665	4	10.3	31	22	AAM71701	Human bone marrow
666	4	10.3	31	22	AAM73303	Human bone marrow
667	4	10.3	31	22	AAM15284	Peptide #1718 enco
668	4	10.3	31	22	AAM16927	Peptide #3361 enco
669	4	10.3	31	22	AAM19230	Peptide #5664 enco
670	4	10.3	31	22	AAM27753	Peptide #1790 enco
671	4	10.3	31	22	AAM29412	Peptide #3449 enco
672	4	10.3	31	22	AAM31899	Peptide #5936 enco
673	4	10.3	31	22	AAM31993	Peptide #6030 enco
674	4	10.3	31	22	AAM33503	Peptide #7540 enco
675	4	10.3	31	22	AAM03033	Peptide #1715 enco
676	4	10.3	31	22	AAM04621	Peptide #3303 enco
677	4	10.3	31	22	AAG77415	Human colon cancer

678	4	10.3	31	22	AAB64588	Human secreted pro
679	4	10.3	31	23	ABP56034	Histidine-tagged p
680	4	10.3	31	23	ABG78091	ITALY, LOR-2, STRI
681	4	10.3	31	23	AAE23925	Human TCR Vbeta17
682	4	10.3	31	23	ABJ01053	Human breast speci
683	4	10.3	31	23	ABG37080	Human peptide enco
684	4	10.3	31	23	ABG38688	Human peptide enco
685	4	10.3	31	23	ABG41414	Human peptide enco
686	4	10.3	31	23	ABG41515	Human peptide enco
687	4	10.3	31	23	ABG43154	Human peptide enco
688	4	10.3	31	23	ABP41445	Human ovarian anti
689	4	10.3	31	23	AAM52295	Miniature protein
690	4	10.3	31	23	AAM52296	Miniature protein
691	4	10.3	31	23	AAM52297	Miniature protein
692	4	10.3	31	23	AAM52298	Miniature protein
693	4	10.3	31	24	ABR00985	Human gene 39-enco
694	4	10.3	31	24	AAG79906	KIAA1819 minimal N
695	4	10.3	31	24	ABP99511	Human secreted pro
696	4	10.3	31	24	ABR00821	Bioactive syntheti
697	4	10.3	31	24	ABP79892	N. gonorrhoeae ami
698	4	10.3	32	12	AAR13836	Mutant signal pept
699	4	10.3	32	13	AAR23648	Antiviral peptide
700	4	10.3	32	15	AAR48260	Mitochondrial matr
701	4	10.3	32	15	AAR57988	B. licheniformis a
702	4	10.3	32	16	AAR74060	Superantigen pepti
703	4	10.3	32	19	AAW66430	Cationic peptide R
704	4	10.3	32	19	AAW66431	Cationic peptide R
705	4	10.3	32	20	AAAY39980	MMTV ORF(245-276)
706	4	10.3	32	20	AAW96358	Mitochondrial matr
707	4	10.3	32	20	AAAY02681	Human secreted pro
708	4	10.3	32	20	AAAY12359	Human 5' EST secre
709	4	10.3	32	20	AAAY12064	Human 5' EST secre
710	4	10.3	32	20	AAW78165	Human secreted pro
711	4	10.3	32	20	AAW73207	Rat defensin-2 pep
712	4	10.3	32	21	AAB39009	Human secreted pep
713	4	10.3	32	21	AAB28704	Human secreted pro
714	4	10.3	32	21	AAB10431	Rat pathogenic pri
715	4	10.3	32	21	AAG55998	Arabidopsis thalia
716	4	10.3	32	21	AAAY91729	Cationic peptide R
717	4	10.3	32	21	AAAY91730	Cationic peptide R
718	4	10.3	32	21	AAAY58894	Polyketide polylin
719	4	10.3	32	21	AAAY54389	Amino acid sequenc
720	4	10.3	32	21	AAAY54397	Amino acid sequenc
721	4	10.3	32	21	AAAY54405	Amino acid sequenc
722	4	10.3	32	22	ABG47791	Human liver peptid
723	4	10.3	32	22	ABG50306	Human liver peptid
724	4	10.3	32	22	AAG77848	Mouse CXCR3 chemok
725	4	10.3	32	22	ABG00577	Novel human diagno
726	4	10.3	32	22	ABG21782	Novel human diagno
727	4	10.3	32	22	ABG26119	Novel human diagno
728	4	10.3	32	22	AAG65882	B. licheniformis a
729	4	10.3	32	22	ABB27768	Human peptide #419
730	4	10.3	32	22	ABB32939	Peptide #445 encod
731	4	10.3	32	22	ABB35446	Peptide #2952 enco
732	4	10.3	32	22	ABB18416	Protein #415 encod
733	4	10.3	32	22	ABB20885	Protein #2884 enco
734	4	10.3	32	22	AAG65199	Human immunodefici

735	4	10.3	32	22	AAG65200	Simian immunodeficient
736	4	10.3	32	22	AAM53740	Human brain expressed
737	4	10.3	32	22	AAM56270	Human brain expressed
738	4	10.3	32	22	AAM66123	Human bone marrow
739	4	10.3	32	22	AAM89561	Human immune/haema
740	4	10.3	32	22	AAM92756	Human digestive system
741	4	10.3	32	22	AAE06938	Human membrane-type
742	4	10.3	32	22	AAM13994	Peptide #428 encoded
743	4	10.3	32	22	AAM16459	Peptide #2893 encoded
744	4	10.3	32	22	AAM26400	Peptide #437 encoded
745	4	10.3	32	22	AAM01735	Peptide #417 encoded
746	4	10.3	32	22	AAM04188	Peptide #2870 encoded
747	4	10.3	32	23	ABG92993	Localisation sequence
748	4	10.3	32	23	ABG30856	Human ornithine transferase
749	4	10.3	32	23	ABG35773	Human peptide encoded
750	4	10.3	32	23	ABB80704	Mouse CXCR3 derived
751	4	10.3	32	23	ABP27640	Streptococcus polydysenteriae
752	4	10.3	32	23	AAU91012	Transplant media associated
753	4	10.3	32	23	AAU91045	Transplant media associated
754	4	10.3	32	23	AAU70444	Mouse light chain
755	4	10.3	32	23	AAG80163	TPR1 protein fragment
756	4	10.3	32	23	AAG80165	TPR2B protein fragment
757	4	10.3	32	23	AAU69725	Cell death protectin
758	4	10.3	32	24	ABR01103	Human gene 157-encoding
759	4	10.3	32	24	ABU59606	Cationic cancer -type
760	4	10.3	32	24	ABU59607	Cationic cancer -type
761	4	10.3	32	24	ABP56588	Mitochondrial matrix
762	4	10.3	32	24	ABP60612	Rat insulin receptor
763	4	10.3	32	24	ABP99621	Human secreted protein
764	4	10.3	32	24	ABP77933	N. gonorrhoeae aminopeptidase
765	4	10.3	32	24	ABP78019	N. gonorrhoeae aminopeptidase
766	4	10.3	32	24	ABU02632	S. pneumoniae type 3
767	4	10.3	33	10	AAP92273	Peptide PF19 from
768	4	10.3	33	11	AAR06628	Bridging sequence
769	4	10.3	33	14	AAR33102	Human cytomegalovirus
770	4	10.3	33	16	AAR82896	Human B7-1 signal
771	4	10.3	33	16	AAR70265	Partial IGF-I fusion
772	4	10.3	33	18	AAW18069	Soluble starch synthase
773	4	10.3	33	19	AAW66429	Cationic peptide N
774	4	10.3	33	19	AAW66423	Cationic peptide M
775	4	10.3	33	19	AAW72585	SSSI maize BE-86 kDa
776	4	10.3	33	19	AAW41866	Peptide used in rat
777	4	10.3	33	19	AAW41867	Peptide used in rat
778	4	10.3	33	20	AAV11807	Human 5' EST secreted
779	4	10.3	33	20	AAW73202	Rabbit defensin-2
780	4	10.3	33	21	AAB56648	Human prostate cancer
781	4	10.3	33	21	AAB56936	Human prostate cancer
782	4	10.3	33	21	AAB27914	Human secreted protein
783	4	10.3	33	21	AAB38653	HIV-1 peptide epitope
784	4	10.3	33	21	AAB38654	HIV-1 peptide epitope
785	4	10.3	33	21	AAB38655	HIV-1 peptide epitope
786	4	10.3	33	21	AAB38656	HIV-1 peptide epitope
787	4	10.3	33	21	AAB38657	HIV-1 peptide epitope
788	4	10.3	33	21	AAB38658	HIV-1 peptide epitope
789	4	10.3	33	21	AAB38960	HIV-1 peptide epitope
790	4	10.3	33	21	AAB45354	Human secreted protein
791	4	10.3	33	21	AAB15479	TCR beta V-N-J region

792	4	10.3	33	21	AAB28706	Human secreted pro
793	4	10.3	33	21	AAB12207	Partial sequence o
794	4	10.3	33	21	AAB12209	Partial sequence o
795	4	10.3	33	21	AAB12210	Partial sequence o
796	4	10.3	33	21	AAB12211	Partial sequence o
797	4	10.3	33	21	AAB12212	Partial sequence o
798	4	10.3	33	21	AAB12213	Partial sequence o
799	4	10.3	33	21	AAB12214	Partial sequence o
800	4	10.3	33	21	AAB12215	Partial sequence o
801	4	10.3	33	21	AAB12216	Partial sequence o
802	4	10.3	33	21	AAB12217	Partial sequence o
803	4	10.3	33	21	AAB12218	Partial sequence o
804	4	10.3	33	21	AAB12220	Partial sequence o
805	4	10.3	33	21	AAB12221	Partial sequence o
806	4	10.3	33	21	AAB12222	Partial sequence o
807	4	10.3	33	21	AAB12224	Partial sequence o
808	4	10.3	33	21	AAB12225	Partial sequence o
809	4	10.3	33	21	AAB12227	Partial sequence o
810	4	10.3	33	21	AAB12228	Partial sequence o
811	4	10.3	33	21	AAB12231	Partial sequence o
812	4	10.3	33	21	AAB12233	Partial sequence o
813	4	10.3	33	21	AAB12234	Partial sequence o
814	4	10.3	33	21	AAB12235	Partial sequence o
815	4	10.3	33	21	AAB12236	Partial sequence o
816	4	10.3	33	21	AAY91722	Cationic peptide M
817	4	10.3	33	21	AAY91728	Cationic peptide N
818	4	10.3	33	21	AAY79839	HIV infection dete
819	4	10.3	33	21	AAY54390	Amino acid sequenc
820	4	10.3	33	21	AAY54398	Amino acid sequenc
821	4	10.3	33	21	AAY54406	Amino acid sequenc
822	4	10.3	33	21	AAY67712	Peptide #112 for d
823	4	10.3	33	21	AAY53944	Peptide representi
824	4	10.3	33	21	AAY56366	Mycobacterium tube
825	4	10.3	33	21	AAY65922	Transcription fact
826	4	10.3	33	22	ABG49373	Human liver peptid
827	4	10.3	33	22	ABG51491	Human liver peptid
828	4	10.3	33	22	ABG52572	Human liver peptid
829	4	10.3	33	22	ABG53813	Human liver peptid
830	4	10.3	33	22	AAU97938	pET20LSCasp3 relat
831	4	10.3	33	22	ABG18683	Novel human diagno
832	4	10.3	33	22	ABG26205	Novel human diagno
833	4	10.3	33	22	ABB29379	Peptide #2030 enco
834	4	10.3	33	22	ABB31428	Peptide #4079 enco
835	4	10.3	33	22	ABB31514	Peptide #4165 enco
836	4	10.3	33	22	ABB34552	Peptide #2058 enco
837	4	10.3	33	22	ABB36641	Peptide #4147 enco
838	4	10.3	33	22	ABB36725	Peptide #4231 enco
839	4	10.3	33	22	ABB37708	Peptide #5214 enco
840	4	10.3	33	22	ABB38907	Peptide #6413 enco
841	4	10.3	33	22	ABB19960	Protein #1959 enco
842	4	10.3	33	22	ABB21975	Protein #3974 enco
843	4	10.3	33	22	ABB23900	Protein #5899 enco
844	4	10.3	33	22	ABB03121	Human musculoskele
845	4	10.3	33	22	AAU21157	Human novel foetal
846	4	10.3	33	22	AAM55339	Human brain expres
847	4	10.3	33	22	AAM57403	Human brain expres
848	4	10.3	33	22	AAM59558	Human brain expres

849	4	10.3	33	22	AAM67735	Human bone marrow
850	4	10.3	33	22	AAM69797	Human bone marrow
851	4	10.3	33	22	AAM70809	Human bone marrow
852	4	10.3	33	22	AAM72127	Human bone marrow
853	4	10.3	33	22	AAM83263	Human immune/haema
854	4	10.3	33	22	AAM86040	Human immune/haema
855	4	10.3	33	22	AAM91722	Human immune/haema
856	4	10.3	33	22	AAO08364	Human polypeptide
857	4	10.3	33	22	AAO13724	Human polypeptide
858	4	10.3	33	22	AAM15546	Peptide #1980 enco
859	4	10.3	33	22	AAM17620	Peptide #4054 enco
860	4	10.3	33	22	AAM17702	Peptide #4136 enco
861	4	10.3	33	22	AAM18651	Peptide #5085 enco
862	4	10.3	33	22	AAM19450	Peptide #5884 enco
863	4	10.3	33	22	AAM28035	Peptide #2072 enco
864	4	10.3	33	22	AAM30138	Peptide #4175 enco
865	4	10.3	33	22	AAM30216	Peptide #4253 enco
866	4	10.3	33	22	AAM32389	Peptide #6426 enco
867	4	10.3	33	22	AAM03295	Peptide #1977 enco
868	4	10.3	33	22	AAM05278	Peptide #3960 enco
869	4	10.3	33	22	AAM05364	Peptide #4046 enco
870	4	10.3	33	22	AAM06258	Peptide #4940 enco
871	4	10.3	33	22	AAE03252	Human gene 4 encod
872	4	10.3	33	22	AAB66616	Mouse prion helix
873	4	10.3	33	22	AAB60711	Human secreted pro
874	4	10.3	33	22	AAB50220	Membrane disruptiv
875	4	10.3	33	23	ABU51880	Helicobacter pylor
876	4	10.3	33	23	AAE30590	Fruit fly odorant
877	4	10.3	33	23	ABJ01093	Ovary cell-specifi
878	4	10.3	33	23	ABG37294	Human peptide enco
879	4	10.3	33	23	ABG39426	Human peptide enco
880	4	10.3	33	23	ABG41941	Human peptide enco
881	4	10.3	33	23	AAU93751	Herpes simplex vir
882	4	10.3	33	23	AAU93752	Herpes simplex vir
883	4	10.3	33	23	AAU93753	Herpes simplex vir
884	4	10.3	33	23	AAU93754	Herpes simplex vir
885	4	10.3	33	23	AAU93755	Herpes simplex vir
886	4	10.3	33	23	AAU93756	Herpes simplex vir
887	4	10.3	33	23	AAU93757	Herpes simplex vir
888	4	10.3	33	23	AAU93758	Herpes simplex vir
889	4	10.3	33	23	AAU93759	Herpes simplex vir
890	4	10.3	33	23	AAU93760	Herpes simplex vir
891	4	10.3	33	23	AAU93761	Herpes simplex vir
892	4	10.3	33	23	AAU93762	Herpes simplex vir
893	4	10.3	33	23	AAU93763	Herpes simplex vir
894	4	10.3	33	23	AAU93764	Herpes simplex vir
895	4	10.3	33	23	AAU93765	Herpes simplex vir
896	4	10.3	33	23	AAU93766	Herpes simplex vir
897	4	10.3	33	23	AAU93767	Herpes simplex vir
898	4	10.3	33	23	AAU93768	Herpes simplex vir
899	4	10.3	33	23	AAU93769	Herpes simplex vir
900	4	10.3	33	23	AAU93770	Herpes simplex vir
901	4	10.3	33	23	AAU93771	Herpes simplex vir
902	4	10.3	33	23	AAU93772	Herpes simplex vir
903	4	10.3	33	23	AAU93773	Herpes simplex vir
904	4	10.3	33	23	AAU93774	Herpes simplex vir
905	4	10.3	33	23	AAU91007	Transplant media a

906	4	10.3	33	23	ABB05812	Amb a I MAJOR amin
907	4	10.3	33	23	ABB05813	Amb a I MINOR amin
908	4	10.3	33	23	ABB05884	Amb a I MAJOR amin
909	4	10.3	33	23	ABB05885	Amb a I MINOR amin
910	4	10.3	33	24	ABU59599	Cationic cancer -t
911	4	10.3	33	24	ABU59605	Cationic cancer -t
912	4	10.3	33	24	ABP58163	Mouse DAKAR ankyri
913	4	10.3	33	24	ABU12415	Novel human muscul
914	4	10.3	33	24	ABU00745	S. pneumoniae type
915	4	10.3	33	24	ABU01120	S. pneumoniae type
916	4	10.3	33	24	ABU01210	S. pneumoniae type
917	4	10.3	34	14	AAR44778	N-terminal sequenc
918	4	10.3	34	15	AAR45511	Parathyroid hormon
919	4	10.3	34	16	AAR85893	WD-40 consensus se
920	4	10.3	34	16	AAR83120	Thermus thermophil
921	4	10.3	34	16	AAR69041	PTH analogue with
922	4	10.3	34	17	AAY16755	Calcitonin peptide
923	4	10.3	34	17	AAR94017	Thermus thermophil
924	4	10.3	34	18	AAW35877	Leader sequence fo
925	4	10.3	34	18	AAW13338	Truncated parathyr
926	4	10.3	34	18	AAW12634	Parathyroid hormon
927	4	10.3	34	18	AAW01812	Human papillomavir
928	4	10.3	34	19	AAW61713	Parathyroid hormon
929	4	10.3	34	19	AAW66039	Parathyroid hormon
930	4	10.3	34	19	AAW42585	Parathyroid hormon
931	4	10.3	34	20	AAY60170	Human endometrium
932	4	10.3	34	20	AAY41508	Fragment of human
933	4	10.3	34	20	AAY48250	Human prostate can
934	4	10.3	34	20	AAW74385	Modified parathyro
935	4	10.3	34	20	AAY00277	Human secreted pro
936	4	10.3	34	20	AAW81931	Synthetic PTH and
937	4	10.3	34	21	AAB52133	Human secreted pro
938	4	10.3	34	21	AAB39261	Gene 23 human secr
939	4	10.3	34	21	AAB44620	Human secreted pro
940	4	10.3	34	21	AAB44734	Human secreted pro
941	4	10.3	34	21	AAB38026	Fragment of human
942	4	10.3	34	21	AAB10375	HSV gD signal pept
943	4	10.3	34	21	AAB16930	Bacteriophage Dp-1
944	4	10.3	34	21	AAY92780	Vtgss-CAT fusion p
945	4	10.3	34	21	AAY58893	Polyketide polylin
946	4	10.3	34	21	AAY54391	Amino acid sequenc
947	4	10.3	34	21	AAY54399	Amino acid sequenc
948	4	10.3	34	21	AAY54407	Amino acid sequenc
949	4	10.3	34	21	AAY58292	Human p160 coactiv
950	4	10.3	34	21	AAY58295	Human p160 coactiv
951	4	10.3	34	21	AAY58298	Human p160 coactiv
952	4	10.3	34	21	AAY58335	Human Grip-1 H17A/
953	4	10.3	34	21	AAY67777	Peptide #177 for d
954	4	10.3	34	21	AAY65921	Transcription fact
955	4	10.3	34	22	ABG49025	Human liver peptid
956	4	10.3	34	22	ABG51121	Human liver peptid
957	4	10.3	34	22	ABG54406	Human liver peptid
958	4	10.3	34	22	ABG58736	Human liver peptid
959	4	10.3	34	22	ABG00686	Novel human diagno
960	4	10.3	34	22	ABG25440	Novel human diagno
961	4	10.3	34	22	ABB29022	Peptide #1673 enco
962	4	10.3	34	22	ABB34186	Peptide #1692 enco

963	4	10.3	34	22	ABB36285	Peptide #3791 enco
964	4	10.3	34	22	ABB39416	Peptide #6922 enco
965	4	10.3	34	22	ABB43350	Peptide #10856 enc
966	4	10.3	34	22	ABB43940	Peptide #11446 enc
967	4	10.3	34	22	ABB19627	Protein #1626 enco
968	4	10.3	34	22	ABB21650	Protein #3649 enco
969	4	10.3	34	22	ABB26347	Protein #8346 enco
970	4	10.3	34	22	ABB26854	Protein #8853 enco
971	4	10.3	34	22	AAM54980	Human brain expres
972	4	10.3	34	22	AAM57056	Human brain expres
973	4	10.3	34	22	AAM60097	Human brain expres
974	4	10.3	34	22	AAM64258	Human brain expres
975	4	10.3	34	22	AAM64933	Human brain expres
976	4	10.3	34	22	AAM67363	Human bone marrow
977	4	10.3	34	22	AAM69446	Human bone marrow
978	4	10.3	34	22	AAM72708	Human bone marrow
979	4	10.3	34	22	AAM77082	Human bone marrow
980	4	10.3	34	22	AAM77668	Human bone marrow
981	4	10.3	34	22	AAM84974	Human immune/haema
982	4	10.3	34	22	AAO09392	Human polypeptide
983	4	10.3	34	22	AAM15194	Peptide #1628 enco
984	4	10.3	34	22	AAM17280	Peptide #3714 enco
985	4	10.3	34	22	AAM21060	Peptide #7494 enco
986	4	10.3	34	22	AAM21588	Peptide #8022 enco
987	4	10.3	34	22	AAM27653	Peptide #1690 enco
988	4	10.3	34	22	AAM29780	Peptide #3817 enco
989	4	10.3	34	22	AAM32939	Peptide #6976 enco
990	4	10.3	34	22	AAM37204	Peptide #11241 enc
991	4	10.3	34	22	AAM37870	Peptide #11907 enc
992	4	10.3	34	22	AAM02934	Peptide #1616 enco
993	4	10.3	34	22	AAM04968	Peptide #3650 enco
994	4	10.3	34	22	AAB84639	Antigenic peptide
995	4	10.3	34	22	AAB62581	Peptide antigen cr
996	4	10.3	34	22	AAB50118	Human brain T calc
997	4	10.3	34	23	ABG70720	Human tetratricope
998	4	10.3	34	23	ABP62013	Human secreted pro
999	4	10.3	34	23	ABB79459	Gene highly expres
1000	4	10.3	34	23	ABG36994	Human peptide enco

ALIGNMENTS

RESULT 1

AAB80490

ID AAB80490 standard; Peptide; 39 AA.

XX

AC AAB80490;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 peptide #1.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;

RESULT 2

ABB82202

ID ABB82202 standard; peptide; 39 AA.

XX

AC ABB82202;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 polypeptide fragment (residues 1-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;

KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;

KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (JUEP/) JUEPPNER H.

PA (GARD/) GARDELLA T J.

PA (JONS/) JONSSON K P.

PA (JOHN/) JOHN M R.

PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT New truncated TIP39 polypeptides and chimeric parathyroid

PT hormone-related peptide/TIP polypeptides, useful as modulators of

PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,

PT hypercalcemia or osteoporosis -

XX

PS Claim 9; Page 79; 112pp; English.

XX

CC The invention relates to truncated TIP39 polypeptide fragments and

CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP

CC polypeptides. The polypeptides are useful as an antagonist of PTH

CC receptors to treat conditions requiring antagonism of parathyroid hormone

CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also

CC useful for treating mammalian conditions characterized by abnormality

CC related to activated PTH2R. It is also useful for treating a mammalian

CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.

CC hyperparathyroidism or hypercalcemia), or characterized by increases in

CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful

CC for treating mammalian conditions characterized by decreases in bone

CC mass, e.g. osteoporosis. The present sequence represents a TIP39

CC polypeptide fragment.

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 23; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

|||||

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 3

AAE23970

ID AAE23970 standard; peptide; 39 AA.

XX

AC AAE23970;

XX

DT 23-SEP-2002 (first entry)

XX

DE Human TIP39 mature protein.

XX

KW Human; tuberoinfundibular peptide; TIP39; signal transduction;

KW parathyroid hormone 2; PTH2 receptor.

XX

OS Homo sapiens.

XX

PN WO200233049-A1.

XX

PD 25-APR-2002.

XX

PF 12-OCT-2001; 2001WO-US31954.

XX

PR 17-OCT-2000; 2000US-241012P.

XX

PA (MERI) MERCK & CO INC.

XX

PI Wang H, Koblan KS, Sun H, Della Penna K;

XX

DR WPI; 2002-471397/50.

DR N-PSDB; AAD38678.

XX

PT Isolated polynucleotide encoding human TIP39 peptide for identifying

PT functional TIP39 and a test compound which modulates the activity of

PT the peptide -

XX

PS Claim 9; Fig 3; 61pp; English.

XX

CC The invention relates to human tuberoinfundibular peptide (TIP39)
CC and nucleic acid molecules encoding such peptides. Polynucleotides
CC of the invention are useful in bioassays for identifying test
CC compounds that modulate the TIP39 activity. TIP39 polypeptides are
CC used for modulating the endogenous signal transducing activity of
CC parathyroid hormone 2 (PTH-2) receptor in a mammal. They are also
CC useful as diagnostics for distinguishing disease states caused by
CC a dysfunctional endogenous TIP39 or PTH-2 receptor and for screening
CC compounds in vitro to determine whether a compound functions as a

CC potential agonist or antagonist. The present sequence is human
CC TIP39 mature protein.

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 23; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 4

ABP56764

ID ABP56764 standard; Protein; 39 AA.

XX

AC ABP56764;

XX

DT 01-APR-2003 (first entry)

XX

DE Human TIP39 protein SEQ ID NO:3.

XX

KW Human; TIP39; tuberoinfundibular peptide of 39 residues; PTH2 receptor;
KW parathyroid hormone 2 receptor; pain; analgesic; chronic pain syndrome;
KW PTH2 receptor modulator; hypersensitivity; windup; allodynia.

XX

OS Homo sapiens.

XX

PN WO2002100349-A2.

XX

PD 19-DEC-2002.

XX

PF 12-JUN-2002; 2002WO-US18771.

XX

PR 13-JUN-2001; 2001US-297959P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin T;

XX

DR WPI; 2003-167369/16.

DR N-PSDB; ABZ22667.

XX

PT Ameliorating pain, e.g. chronic pain syndromes, hypersensitivity,
PT windup or allodynia, comprises administering a modulator of the
PT parathyroid hormone-2 (PTH2) receptor -

XX

PS Disclosure; Page 5; 56pp; English.

XX

CC The present invention describes a method for ameliorating pain. The
CC method comprises administering a compound that modulates a parathyroid
CC hormone-2 (PTH2) receptor to a patient. Tuberoinfundibular peptide of 39
CC residues (TIP39) selectively activates the PTH2 receptor. TIP39 has
CC analgesic activity, and can be used as a PTH2 receptor modulator. The
CC method is useful for ameliorating pain in a patient, e.g. chronic pain

CC syndromes, hypersensitivity, windup or allodynia. The present sequence
CC represents human TIP39, which is given in the exemplification of the
CC present invention.

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

||||||||||||||||||||||||||||||||||||||||

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 5

AAU73181

ID AAU73181 standard; Peptide; 40 AA.

XX

AC AAU73181;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #163.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

The invention relates to a composition (I) comprising modulators of parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP) which comprise a PTH/PTHrP modulating domain and a vehicle. (I) comprising PTH agonist optionally with a bone resorption inhibitor, such as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates, oestrogens, oestrogen receptor modulators and tibolone is useful for treating osteopenia. (I) is useful for therapeutic and prophylactic purposes. Antagonists of PTH receptor are useful in treating primary and secondary hyperthyroidism, hypercalcaemia, tumour metastases, particularly breast and prostate cancer, cachexia and anorexia, osteopenia, including various forms of osteoporosis, Paget's disease of bone, osteomyelitis, osteonecrosis or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease and alopecia. PTH receptor agonists are useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone and parathyroid hormone related protein (PTH/PTHrP) modulators and related amino acid sequences of the invention.

SO Sequence 40 AA;

Query Match 100.0%; Score 39; DB 23; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 6

AAB80489

ID AAB80489 standard; Peptide; 38 AA.

XX

AC AAB80489;

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #2.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

05 Bos taurus.

OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 16; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 38 AA;

Query Match 97.4%; Score 38; DB 22; Length 38;
 Best Local Similarity 100.0%; Pred. No. 4.8e-27;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 ||||||||||||||||||||||||||||||||||||
 Db 1 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 38

RESULT 7
 AAB80526
 ID AAB80526 standard; Peptide; 38 AA.
 XX
 AC AAB80526;
 XX

DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #38.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX

CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.

XX
 SQ Sequence 37 AA;

Query Match 94.9%; Score 37; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 37

RESULT 9

AAB80525

ID AAB80525 standard; Peptide; 37 AA.

XX

AC AAB80525;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #39.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiastatic, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 37 AA;

Query Match 94.9%; Score 37; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLD 37
 |||||
 Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLD 37

RESULT 10

ABB82197

ID ABB82197 standard; peptide; 37 AA.

XX

AC ABB82197;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 truncated peptide fragment (residues 3-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;

KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;

KW hypercalcemia; osteoporosis.
 XX
 OS Bos sp.
 XX
 PN WO200268585-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 17-JAN-2002; 2002WO-US01183.
 XX
 PR 17-JAN-2001; 2001US-261804P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (JUEP/) JUEPPNER H.
 PA (GARD/) GARDELLA T J.
 PA (JONS/) JONSSON K P.
 PA (JOHN/) JOHN M R.
 PA (GENS/) GENSURE R C.
 XX
 PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;
 XX
 DR WPI; 2002-713370/77.
 XX
 PT New truncated TIP39 polypeptides and chimeric parathyroid
 PT hormone-related peptide/TIP polypeptides, useful as modulators of
 PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
 PT hypercalcemia or osteoporosis -
 XX
 PS Claim 1; Page 78; 112pp; English.
 XX
 CC The invention relates to truncated TIP39 polypeptide fragments and
 CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
 CC polypeptides. The polypeptides are useful as an antagonist of PTH
 CC receptors to treat conditions requiring antagonism of parathyroid hormone
 CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
 CC useful for treating mammalian conditions characterized by abnormality
 CC related to activated PTH2R. It is also useful for treating a mammalian
 CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
 CC hyperparathyroidism or hypercalcemia), or characterized by increases in
 CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
 CC for treating mammalian conditions characterized by decreases in bone
 CC mass, e.g. osteoporosis. The present sequence represents a truncated
 CC TIP39 polypeptide fragment.
 XX
 SQ Sequence 37 AA;

Query Match 94.9%; Score 37; DB 23; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 37

ID AAB80487 standard; Peptide; 36 AA.
XX
AC AAB80487;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #4.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating

XX
 PS Claim 5; Page 17; 106pp; English.
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 CC The present invention describes an isolated or purified peptide (I) that
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 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
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 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 36 AA;

Query Match 92.3%; Score 36; DB 22; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.9e-25;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36
 |||||
 Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36

RESULT 13

AAB80486

ID AAB80486 standard; Peptide; 35 AA.

XX

AC AAB80486;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #5.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
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 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 35 AA;

Query Match 89.7%; Score 35; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.2e-24;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 35

RESULT 14
 AAB80523
 ID AAB80523 standard; Peptide; 35 AA.
 XX
 AC AAB80523;
 XX
 DT 26-APR-2001 (first entry)
 XX

DE PTH2 receptor binding activity TIP39 truncation peptide #41.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
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PD 21-DEC-2000.
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PI Usdin TB, Hoare SRJ;
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DR WPI; 2001-122833/13.
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CC hypertension, congestive heart failure and control of tumour growth,
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CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 35 AA;

Query Match 89.7%; Score 35; DB 22; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35
|||||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35

RESULT 15

AAB80527

ID AAB80527 standard; Peptide; 35 AA.

XX

AC AAB80527;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #74.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

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PF 15-JUN-2000; 2000WO-US16776.

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PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

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DR WPI; 2001-122833/13.

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PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
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PS Claim 6; Page 17; 106pp; English.

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 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
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 SQ Sequence 35 AA;

Query Match 89.7%; Score 35; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.2e-24;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 35

RESULT 16

AAB80485

ID AAB80485 standard; Peptide; 34 AA.

XX

AC AAB80485;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #6.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

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PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.
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 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
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 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
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 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 34 AA;

Query Match 87.2%; Score 34; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 34

RESULT 17

AAB80522

ID AAB80522 standard; Peptide; 34 AA.

XX

AC AAB80522;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #42.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;

KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
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 PF 15-JUN-2000; 2000WO-US16776.
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 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
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 DR WPI; 2001-122833/13.
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 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
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 CC activities, and is an PTH receptor antagonist. The peptide is useful in
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 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 34 AA;

Query Match 87.2%; Score 34; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34
 ||||||||||||||||||||||||||||

Db

1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34

RESULT 18

AAB80528

ID AAB80528 standard; Peptide; 34 AA.

XX

AC AAB80528;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #75.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

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PF 15-JUN-2000; 2000WO-US16776.

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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

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PI Usdin TB, Hoare SRJ;

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DR WPI; 2001-122833/13.

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 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 34 AA;

Query Match 87.2%; Score 34; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 34

RESULT 19

AAB80484

ID AAB80484 standard; Peptide; 33 AA.

XX

AC AAB80484;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #7.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
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 KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

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PD 21-DEC-2000.

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PF 15-JUN-2000; 2000WO-US16776.

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PI Usdin TB, Hoare SRJ;

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DR WPI; 2001-122833/13.
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 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 33 AA;

Query Match 84.6%; Score 33; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 33

RESULT 20

AAB80521

ID AAB80521 standard; Peptide; 33 AA.

XX

AC AAB80521;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #43.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
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 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
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 XX
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 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
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 XX
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Query Match 84.6%; Score 33; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33
 ||||||||||||||||||||||||||||||||||||
 Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33

RESULT 21
 AAB80529
 ID AAB80529 standard; Peptide; 33 AA.

XX
 AC AAB80529;
 XX
 DT 26-APR-2001 (first entry)
 XX
 DE PTH2 receptor binding activity TIP39 truncation peptide #76.
 XX
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 6; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to

CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

50 Sequence 33 AA;

Query Match 84.6%; Score 33; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||
 Db 1 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 33

RESULT 22

ID AAB80483 standard; Peptide; 32 AA.

AC AAB80483;

DT 26-APR-2001 (first entry)

DE PTH2 receptor binding activity TIP39 truncation peptide #8.

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiact;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

OS Bos taurus.

OS Synthetic.

PN WO200077042-A2.

PD 21-DEC-2000.

PF 15-JUN-2000; 2000WO-US16776.

PR 15-JUN-1999; 99US-0139335.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Usdin TB, Hoare SRJ;

DR WPI; 2001-122833/13.

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

[illegible]

Sequence 32 AA;

Qy 8 AAFRERARLLAALERHRLNSYMHKLLVLDP 39
 |||||
 Db 1 AAFRERARLLAALERHRLNSYMHKLLVLDP 32

AAB80520

[illegible]

26-APR-2001 (first entry)

Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand; parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic; antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic; cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; depression; schizophrenia; dementia; acute pain; chronic pain; migraine; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; congestive heart failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis; leukodystrophy.

Synthetic.

WO200077042-A2.

XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 32 AA;

Query Match 82.1%; Score 32; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.9e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32
 |||||
 Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32

RESULT 24

AAB80530

ID AAB80530 standard; Peptide; 32 AA.

XX

AC AAB80530;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #77.

XX
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 6; Page 18; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 32 AA;

Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 32

RESULT 25

ABB82198

ID ABB82198 standard; peptide; 32 AA.

XX

AC ABB82198;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 truncated peptide fragment (residues 8-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;

KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;

KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (JUEP/) JUEPPNER H.

PA (GARD/) GARDELLA T J.

PA (JONS/) JONSSON K P.

PA (JOHN/) JOHN M R.

PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT New truncated TIP39 polypeptides and chimeric parathyroid

PT hormone-related peptide/TIP polypeptides, useful as modulators of

PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,

PT hypercalcemia or osteoporosis -

XX

PS Claim 2; Page 78; 112pp; English.

XX

CC The invention relates to truncated TIP39 polypeptide fragments and

CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP

CC polypeptides. The polypeptides are useful as an antagonist of PTH

CC receptors to treat conditions requiring antagonism of parathyroid hormone

CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also

CC useful for treating mammalian conditions characterized by abnormality

CC related to activated PTH2R. It is also useful for treating a mammalian

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 31 AA;

Query Match 79.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 AFRERARLLAALERRHWLNSYMHKLLVLDAP 31

RESULT 27

AAB80519

ID AAB80519 standard; Peptide; 31 AA.

XX

AC AAB80519;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #45.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 31 AA;

Query Match 79.5%; Score 31; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.6e-21;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMH 31
 |||||
 Db 1 SLALADDAAFRERARLLAALERRHWLNSYMH 31

RESULT 28

AAB80531

ID AAB80531 standard; Peptide; 31 AA.

XX

AC AAB80531;

XX
 DT 26-APR-2001 (first entry)
 XX
 DE PTH2 receptor binding activity TIP39 truncation peptide #78.
 XX
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 6; Page 18; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.

SQ Sequence 31 AA;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 AFRRERARLLAALERRHWLNSYMHKLLVLDAP 31
```

RESULT 29

ABB82196

ID ABB82196 standard; peptide; 31 AA.

XX

AC ABB82196;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 truncated peptide fragment (residues 9-39).

XX

KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.

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PA (JONS/) JONSSON K P.

PA (JOHN/) JOHN M R.

PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT	hypercalcemia or osteoporosis	-
----	-------------------------------	---

XV

PS Claim 1; Page 78; 112pp; English.

XV

CC polypeptides. The polypeptides are useful as an antagonist of PTH

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 5; Page 16; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiastatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 30 AA;

Query Match 76.9%; Score 30; DB 22; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.8e-20;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39

|||||

Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 31

AAB80518

ID AAB80518 standard; Peptide; 30 AA.

XX

AC AAB80518;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #46.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiastatic;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;

AAB80532

ID AAB80532 standard; Peptide; 30 AA.

XX

AC AAB80532;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #79.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 18; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 5; Page 16; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39

|||||

Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 35

AAB80517

ID AAB80517 standard; Peptide; 29 AA.

XX

AC AAB80517;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #47.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;

KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 22; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSY 29
 |||||

Db 1 SLALADDAAFRERARLLAALERRHWLNSY 29

RESULT 36

AAB80533

ID AAB80533 standard; Peptide; 29 AA.

XX

AC AAB80533;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #80.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 18; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,

PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -
XX
PS Claim 2; Page 78; 112pp; English.
XX
CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.
XX
SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 23; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 38

AAB80479

ID AAB80479 standard; Peptide; 28 AA.

XX

AC AAB80479;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #12.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
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 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
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 PS Claim 5; Page 16; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
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 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiastatic, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 28 AA;

Query Match 71.8%; Score 28; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ERARLLAALERRHWLNSYMHKLLVLDAP 28

RESULT 39
 AAB80516

ID AAB80516 standard; Peptide; 28 AA.
 XX
 AC AAB80516;
 XX
 DT 26-APR-2001 (first entry)
 XX
 DE PTH2 receptor binding activity TIP39 truncation peptide #48.
 XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN WO200077042-A2.
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 PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16776.
 XX
 PR 15-JUN-1999; 99US-0139335.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Usdin TB, Hoare SRJ;
 XX
 DR WPI; 2001-122833/13.
 XX
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX
 PS Claim 5; Page 17; 106pp; English.
 XX
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
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 CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
 CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
 CC truncated peptides which have PTH2 receptor binding activity.
 XX
 SQ Sequence 28 AA;

Query Match 71.8%; Score 28; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.4e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNS 28
|||||||
Db 1 SLALADDAAFRERARLLAALERRHWLNS 28

RESULT 40

AAB80534

ID AAB80534 standard; Peptide; 28 AA.

XX

AC AAB80534;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #81.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

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PR 15-JUN-1999; 99US-0139335.

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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
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PS Claim 6; Page 18; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
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CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 13.243 Seconds
 (without alignments)
 124.604 Million cell updates/sec

Title: US-09-843-221A-170
 Perfect score: 39
 Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score						
1	6	15.4	28	3	US-09-041-886-53	Sequence 53, Appl	
2	6	15.4	37	4	US-08-817-441-7	Sequence 7, Appli	
3	6	15.4	40	3	US-08-894-699-36	Sequence 36, Appl	
4	6	15.4	40	3	US-08-894-699-37	Sequence 37, Appl	
5	6	15.4	40	3	US-08-894-699-39	Sequence 39, Appl	
6	6	15.4	40	3	US-08-894-699-40	Sequence 40, Appl	
7	6	15.4	40	3	US-08-894-699-68	Sequence 68, Appl	
8	6	15.4	40	3	US-09-444-410-36	Sequence 36, Appl	
9	6	15.4	40	3	US-09-444-410-37	Sequence 37, Appl	
10	6	15.4	40	3	US-09-444-410-39	Sequence 39, Appl	
11	6	15.4	40	3	US-09-444-410-40	Sequence 40, Appl	

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16	5	12.8	28	3	US-09-041-886-40	Sequence 40, Appl
17	5	12.8	28	3	US-09-041-886-54	Sequence 54, Appl
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20	5	12.8	34	3	US-08-704-856C-3	Sequence 3, Appli
21	5	12.8	34	4	US-09-242-881-3	Sequence 3, Appli
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51	4	10.3	29	1	US-07-746-705A-3	Sequence 3, Appli
52	4	10.3	29	1	US-08-029-402-19	Sequence 19, Appl
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83	4	10.3	29	4	US-09-699-684-12	Sequence 12, Appl
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552	4	10.3	38	5	PCT-US96-10041-23	Sequence 23, Appl
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573	4	10.3	40	1	US-08-457-865-5	Sequence 5, Appli
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597	4	10.3	40	4	US-08-706-054A-11	Sequence 11, Appl
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659	3	7.7	28	1	US-07-963-321-12	Sequence 12, Appl
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674	3	7.7	28	1	US-08-243-082-1	Sequence 1, Appli
675	3	7.7	28	1	US-08-246-572-4	Sequence 4, Appli
676	3	7.7	28	1	US-08-246-572-5	Sequence 5, Appli
677	3	7.7	28	1	US-08-164-151-22	Sequence 22, Appl
678	3	7.7	28	1	US-08-361-443-1	Sequence 1, Appli
679	3	7.7	28	1	US-08-276-213-4	Sequence 4, Appli
680	3	7.7	28	1	US-07-949-797B-1	Sequence 1, Appli
681	3	7.7	28	1	US-08-182-175A-1	Sequence 1, Appli
682	3	7.7	28	1	US-08-457-605-4	Sequence 4, Appli
683	3	7.7	28	1	US-08-194-591-1	Sequence 1, Appli
684	3	7.7	28	1	US-08-194-591-2	Sequence 2, Appli
685	3	7.7	28	1	US-08-257-446-6	Sequence 6, Appli
686	3	7.7	28	1	US-07-977-630-39	Sequence 39, Appl
687	3	7.7	28	1	US-07-977-630-44	Sequence 44, Appl
688	3	7.7	28	1	US-07-977-630-45	Sequence 45, Appl
689	3	7.7	28	1	US-07-977-630-46	Sequence 46, Appl
690	3	7.7	28	1	US-07-977-630-48	Sequence 48, Appl
691	3	7.7	28	1	US-07-977-630-52	Sequence 52, Appl
692	3	7.7	28	1	US-07-977-630-53	Sequence 53, Appl
693	3	7.7	28	1	US-08-350-884-36	Sequence 36, Appl
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695	3	7.7	28	1	US-08-366-591-12	Sequence 12, Appl

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699	3	7.7	28	1	US-08-056-200-14	Sequence 14, Appl
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705	3	7.7	28	1	US-08-053-131-98	Sequence 98, Appl
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707	3	7.7	28	1	US-08-473-334B-10	Sequence 10, Appl
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713	3	7.7	28	1	US-08-473-334B-16	Sequence 16, Appl
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717	3	7.7	28	1	US-08-473-334B-22	Sequence 22, Appl
718	3	7.7	28	1	US-08-473-334B-23	Sequence 23, Appl
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725	3	7.7	28	1	US-08-308-729-24	Sequence 24, Appl
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727	3	7.7	28	1	US-08-308-729-26	Sequence 26, Appl
728	3	7.7	28	1	US-08-308-729-59	Sequence 59, Appl
729	3	7.7	28	1	US-08-308-729-61	Sequence 61, Appl
730	3	7.7	28	1	US-08-308-729-62	Sequence 62, Appl
731	3	7.7	28	1	US-08-308-729-64	Sequence 64, Appl
732	3	7.7	28	1	US-08-457-865-17	Sequence 17, Appl
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738	3	7.7	28	1	US-08-786-748A-1	Sequence 1, Appli
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746	3	7.7	28	1	US-08-786-748A-26	Sequence 26, Appl
747	3	7.7	28	1	US-08-786-748A-27	Sequence 27, Appl
748	3	7.7	28	1	US-08-786-748A-161	Sequence 161, App
749	3	7.7	28	1	US-08-786-748A-162	Sequence 162, App
750	3	7.7	28	1	US-08-786-748A-163	Sequence 163, App
751	3	7.7	28	1	US-08-786-748A-164	Sequence 164, App
752	3	7.7	28	1	US-08-786-748A-165	Sequence 165, App

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769	3	7.7	28	1	US-08-519-180-2	Sequence 2, Appli
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776	3	7.7	28	1	US-08-449-317A-81	Sequence 81, Appl
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778	3	7.7	28	2	US-08-477-022-81	Sequence 81, Appl
779	3	7.7	28	2	US-08-449-447-81	Sequence 81, Appl
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788	3	7.7	28	2	US-08-908-597A-30	Sequence 30, Appl
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791	3	7.7	28	2	US-08-679-405-8	Sequence 8, Appli
792	3	7.7	28	2	US-08-596-387B-105	Sequence 105, App
793	3	7.7	28	2	US-08-744-139-21	Sequence 21, Appl
794	3	7.7	28	2	US-08-184-328-81	Sequence 81, Appl
795	3	7.7	28	2	US-08-637-759B-489	Sequence 489, App
796	3	7.7	28	2	US-08-308-865-98	Sequence 98, Appl
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804	3	7.7	28	2	US-08-620-151-74	Sequence 74, Appl
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813	3	7.7	28	2	US-08-932-682-18	Sequence 18, Appl
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816	3	7.7	28	2	US-08-932-682-26	Sequence 26, Appl
817	3	7.7	28	2	US-08-932-682-27	Sequence 27, Appl
818	3	7.7	28	2	US-08-932-682-161	Sequence 161, App
819	3	7.7	28	2	US-08-932-682-162	Sequence 162, App
820	3	7.7	28	2	US-08-932-682-163	Sequence 163, App
821	3	7.7	28	2	US-08-932-682-164	Sequence 164, App
822	3	7.7	28	2	US-08-932-682-165	Sequence 165, App
823	3	7.7	28	2	US-08-932-682-169	Sequence 169, App
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827	3	7.7	28	2	US-08-726-306A-132	Sequence 132, App
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833	3	7.7	28	2	US-08-413-708B-2	Sequence 2, Appli
834	3	7.7	28	2	US-08-563-892A-5	Sequence 5, Appli
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841	3	7.7	28	2	US-08-818-253-37	Sequence 37, Appl
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843	3	7.7	28	2	US-08-897-624-2	Sequence 2, Appli
844	3	7.7	28	2	US-08-924-695A-36	Sequence 36, Appl
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846	3	7.7	28	3	US-08-938-548B-4	Sequence 4, Appli
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853	3	7.7	28	3	US-08-486-099-87	Sequence 87, Appl
854	3	7.7	28	3	US-08-486-099-131	Sequence 131, App
855	3	7.7	28	3	US-08-486-099-133	Sequence 133, App
856	3	7.7	28	3	US-08-486-099-161	Sequence 161, App
857	3	7.7	28	3	US-08-433-522A-38	Sequence 38, Appl
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861	3	7.7	28	3	US-09-273-685-49	Sequence 49, Appl
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863	3	7.7	28	3	US-08-360-107A-94	Sequence 94, Appl
864	3	7.7	28	3	US-08-360-107A-96	Sequence 96, Appl
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868	3	7.7	28	3	US-08-484-223B-87	Sequence 87, Appl
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870	3	7.7	28	3	US-08-484-223B-133	Sequence 133, App
871	3	7.7	28	3	US-08-484-223B-161	Sequence 161, App
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878	3	7.7	28	3	US-08-952-568-5	Sequence 5, Appli
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880	3	7.7	28	3	US-08-952-568-7	Sequence 7, Appli
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884	3	7.7	28	3	US-08-952-568-12	Sequence 12, Appl
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886	3	7.7	28	3	US-08-952-568-14	Sequence 14, Appl
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894	3	7.7	28	3	US-08-919-597-133	Sequence 133, App
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898	3	7.7	28	3	US-08-475-668A-86	Sequence 86, Appl
899	3	7.7	28	3	US-08-475-668A-87	Sequence 87, Appl
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902	3	7.7	28	3	US-08-475-668A-161	Sequence 161, App
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905	3	7.7	28	3	US-08-485-551A-86	Sequence 86, Appl
906	3	7.7	28	3	US-08-485-551A-87	Sequence 87, Appl
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909	3	7.7	28	3	US-08-485-551A-161	Sequence 161, App
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912	3	7.7	28	3	US-08-467-023-82	Sequence 82, Appl
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915	3	7.7	28	3	US-08-467-023-217	Sequence 217, App
916	3	7.7	28	3	US-08-467-023-218	Sequence 218, App
917	3	7.7	28	3	US-08-467-023-219	Sequence 219, App
918	3	7.7	28	3	US-08-467-023-223	Sequence 223, App
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921	3	7.7	28	3	US-08-471-913A-87	Sequence 87, Appl
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923	3	7.7	28	3	US-08-471-913A-133	Sequence 133, App

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931	3	7.7	28	3	US-08-893-749-32	Sequence 32, Appl
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933	3	7.7	28	3	US-08-822-324-23	Sequence 23, Appl
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935	3	7.7	28	3	US-09-433-428D-62	Sequence 62, Appl
936	3	7.7	28	3	US-08-793-624-13	Sequence 13, Appl
937	3	7.7	28	3	US-08-796-899-30	Sequence 30, Appl
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939	3	7.7	28	3	US-08-974-549A-235	Sequence 235, App
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945	3	7.7	28	3	US-08-817-811-17	Sequence 17, Appl
946	3	7.7	28	3	US-08-817-811-67	Sequence 67, Appl
947	3	7.7	28	3	US-08-818-252-22	Sequence 22, Appl
948	3	7.7	28	3	US-08-818-252-37	Sequence 37, Appl
949	3	7.7	28	3	US-08-363-558-1	Sequence 1, Appli
950	3	7.7	28	3	US-09-253-396A-221	Sequence 221, App
951	3	7.7	28	3	US-09-253-396A-229	Sequence 229, App
952	3	7.7	28	3	US-09-236-385A-9	Sequence 9, Appli
953	3	7.7	28	3	US-09-236-385A-30	Sequence 30, Appl
954	3	7.7	28	3	US-08-905-223-357	Sequence 357, App
955	3	7.7	28	3	US-08-957-001B-25	Sequence 25, Appl
956	3	7.7	28	3	US-08-485-264A-84	Sequence 84, Appl
957	3	7.7	28	3	US-08-485-264A-86	Sequence 86, Appl
958	3	7.7	28	3	US-08-485-264A-87	Sequence 87, Appl
959	3	7.7	28	3	US-08-485-264A-131	Sequence 131, App
960	3	7.7	28	3	US-08-485-264A-133	Sequence 133, App
961	3	7.7	28	3	US-08-485-264A-161	Sequence 161, App
962	3	7.7	28	3	US-08-485-264A-211	Sequence 211, App
963	3	7.7	28	3	US-09-303-323-37	Sequence 37, Appl
964	3	7.7	28	3	US-09-303-323-74	Sequence 74, Appl
965	3	7.7	28	3	US-09-177-249-73	Sequence 73, Appl
966	3	7.7	28	3	US-09-248-588-42	Sequence 42, Appl
967	3	7.7	28	3	US-08-907-739-8	Sequence 8, Appli
968	3	7.7	28	3	US-09-041-886-50	Sequence 50, Appl
969	3	7.7	28	3	US-09-041-886-56	Sequence 56, Appl
970	3	7.7	28	3	US-09-127-680-2	Sequence 2, Appli
971	3	7.7	28	3	US-08-995-369-1	Sequence 1, Appli
972	3	7.7	28	3	US-09-171-654-1	Sequence 1, Appli
973	3	7.7	28	3	US-09-496-301-25	Sequence 25, Appl
974	3	7.7	28	3	US-09-482-612-5	Sequence 5, Appli
975	3	7.7	28	3	US-09-082-279B-8	Sequence 8, Appli
976	3	7.7	28	3	US-09-082-279B-12	Sequence 12, Appl
977	3	7.7	28	3	US-09-082-279B-14	Sequence 14, Appl
978	3	7.7	28	3	US-09-082-279B-50	Sequence 50, Appl
979	3	7.7	28	3	US-09-082-279B-54	Sequence 54, Appl
980	3	7.7	28	3	US-09-082-279B-63	Sequence 63, Appl

981	3	7.7	28	3	US-09-082-279B-68	Sequence 68, Appl
982	3	7.7	28	3	US-09-082-279B-75	Sequence 75, Appl
983	3	7.7	28	3	US-09-082-279B-82	Sequence 82, Appl
984	3	7.7	28	3	US-09-082-279B-231	Sequence 231, App
985	3	7.7	28	3	US-09-082-279B-673	Sequence 673, App
986	3	7.7	28	3	US-09-082-279B-674	Sequence 674, App
987	3	7.7	28	3	US-09-082-279B-675	Sequence 675, App
988	3	7.7	28	3	US-09-082-279B-676	Sequence 676, App
989	3	7.7	28	3	US-09-082-279B-836	Sequence 836, App
990	3	7.7	28	3	US-09-082-279B-891	Sequence 891, App
991	3	7.7	28	3	US-09-082-279B-908	Sequence 908, App
992	3	7.7	28	3	US-09-082-279B-909	Sequence 909, App
993	3	7.7	28	3	US-09-082-279B-910	Sequence 910, App
994	3	7.7	28	3	US-09-082-279B-911	Sequence 911, App
995	3	7.7	28	3	US-09-082-279B-914	Sequence 914, App
996	3	7.7	28	3	US-09-082-279B-915	Sequence 915, App
997	3	7.7	28	3	US-09-082-279B-958	Sequence 958, App
998	3	7.7	28	3	US-09-082-279B-982	Sequence 982, App
999	3	7.7	28	3	US-09-082-279B-1029	Sequence 1029, Ap
1000	3	7.7	28	4	US-09-442-989-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-041-886-53

; Sequence 53, Application US/09041886

; Patent No. 6235872

; GENERAL INFORMATION:

; APPLICANT: Bredesen, Dale E.

; APPLICANT: Rabizadeh, Sharroz

; TITLE OF INVENTION: Proapoptotic Peptides, Dependence

; TITLE OF INVENTION: Polypeptides and Methods of Use

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/041,886

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 2626

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-53

Query Match 15.4%; Score 6; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAALE 21
 |||||
Db 21 LLAALE 26

RESULT 2

US-08-817-441-7

; Sequence 7, Application US/08817441

; Patent No. 6399294

; GENERAL INFORMATION:

; APPLICANT: CHARNEAU, PIERRE

; APPLICANT: CLAVEL, FRANCOISE

; APPLICANT: BORMAN, ANDREW

; APPLICANT: QUILLIENT, CAROLINE

; APPLICANT: GUETARD, DENISE

; APPLICANT: MONTAGNIER, LUC

; APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE

; APPLICANT: COHEN, JACQUES

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR

; TITLE OF INVENTION: SUBTYPE) ANTIGENS

; NUMBER OF SEQUENCES: 103

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner, L.L.P.

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,441

; FILING DATE: 11-JUL-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR 95/01391

; FILING DATE: 20-OCT-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9412554

; FILING DATE: 20-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9502526
 ; FILING DATE: 03-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 03260.6005-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 37 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-817-441-7

Query Match 15.4%; Score 6; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||
 Db 1 RARLLA 6

RESULT 3

US-08-894-699-36

; Sequence 36, Application US/08894699
 ; Patent No. 6030769

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS
 ; APPLICANT: SARAGOSTI, SENTOB
 ; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
 ; APPLICANT: LY, THOAI-DUONG
 ; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 ; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 ; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 ; STREET: FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/894,699
 ; FILING DATE: 01-DEC-1997

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-36

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Query Match          15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      13 RARLLA 18
        |||||
Db      4 RARLLA 9

```

RESULT 4

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US-08-894-699-37
; Sequence 37, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/894,699
;   FILING DATE:  01-DEC-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/FR96/00294
;   FILING DATE:  26-FEB-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  FR 95/02236
;   FILING DATE:  27-FEB-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  OBLON, NORMAN F.
;   REGISTRATION NUMBER:  24,614
;   REFERENCE/DOCKET NUMBER:  0354-0020-0PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-413-3000
;   TELEFAX:  703-413-2220
;   INFORMATION FOR SEQ ID NO:  37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  40 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-894-699-37

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```

Query Match          15.4%;  Score 6;  DB 3;  Length 40;
Best Local Similarity 100.0%;  Pred. No. 57;
Matches      6;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      13 RARLLA 18
        |||||
Db      4 RARLLA 9

```

RESULT 5

US-08-894-699-39

; Sequence 39, Application US/08894699

; Patent No. 6030769

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARAGOSTI, SENTOB

; APPLICANT: LOUSSERT-AJAKA, IBITISSAM

; APPLICANT: LY, THOAI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; TITLE OF INVENTION: VIRUSES, AND USES THEREOF

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

; STREET: FLOOR

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/894,699
 ; FILING DATE: 01-DEC-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR96/00294
 ; FILING DATE: 26-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 95/02236
 ; FILING DATE: 27-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,614
 ; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-894-699-39

Query Match 15.4%; Score 6; DB 3; Length 40;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||
 Db 4 RARLLA 9

RESULT 6

US-08-894-699-40

; Sequence 40, Application US/08894699
 ; Patent No. 6030769
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMON, FRANCOIS
 ; APPLICANT: SARAGOSTI, SENTOB
 ; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
 ; APPLICANT: LY, THOAI-DUONG
 ; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 ; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 ; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 ; STREET: FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/894,699
 ; FILING DATE: 01-DEC-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR96/00294
 ; FILING DATE: 26-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 95/02236
 ; FILING DATE: 27-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,614
 ; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-894-699-40

Query Match 15.4%; Score 6; DB 3; Length 40;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||
 Db 4 RARLLA 9

RESULT 7

US-08-894-699-68
 ; Sequence 68, Application US/08894699
 ; Patent No. 6030769
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMON, FRANCOIS
 ; APPLICANT: SARAGOSTI, SENTOB
 ; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
 ; APPLICANT: LY, THOAI-DUONG
 ; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

```

; TITLE OF INVENTION:  GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION:  VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES:  81
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE:  P.C.
;   STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
;   STREET:  FLOOR
;   CITY:  ARLINGTON
;   STATE:  VA
;   COUNTRY:  USA
;   ZIP:  22202
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/894,699
;   FILING DATE:  01-DEC-1997
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/FR96/00294
;   FILING DATE:  26-FEB-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  FR 95/02236
;   FILING DATE:  27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME:  OBLON, NORMAN F.
;   REGISTRATION NUMBER:  24,614
;   REFERENCE/DOCKET NUMBER:  0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-413-3000
;   TELEFAX:  703-413-2220
; INFORMATION FOR SEQ ID NO:  68:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  40 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-894-699-68

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```

Query Match          15.4%;  Score 6;  DB 3;  Length 40;
Best Local Similarity 100.0%;  Pred. No. 57;
Matches      6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      13 RARLLA 18
        |||||
Db      4 RARLLA 9

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```

RESULT 8
US-09-444-410-36
; Sequence 36, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:

```

```

; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
;   STREET: FLOOR
;   CITY: ARLINGTON
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22202
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/444,410
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/894,699
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: FR 95/02236
;   FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.
;   REGISTRATION NUMBER: 24,614
;   REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-413-3000
;   TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 40 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-444-410-36

```

```

Query Match          15.4%;  Score 6;  DB 3;  Length 40;
Best Local Similarity 100.0%;  Pred. No. 57;
Matches      6;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      13 RARLLA 18
        |||||
Db      4 RARLLA 9

```

RESULT 9

US-09-444-410-37

; Sequence 37, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-37

Query Match 15.4%; Score 6; DB 3; Length 40;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
| | | | |
Db 4 RARLLA 9

RESULT 10

US-09-444-410-39

; Sequence 39, Application US/09444410

; Patent No. 6270975

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARAGOSTI, SENTOB

; APPLICANT: LOUSSERT-AJAKA, IBITISSAM

; APPLICANT: LY, THOAI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; TITLE OF INVENTION: VIRUSES, AND USES THEREOF

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

; STREET: FLOOR

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,410

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/894,699

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,614

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-444-410-39

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 4 RARLLA 9

RESULT 11

US-09-444-410-40

; Sequence 40, Application US/09444410

; Patent No. 6270975

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARAGOSTI, SENTOB

; APPLICANT: LOUSSERT-AJAKA, IBITISSAM

; APPLICANT: LY, THOAI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; TITLE OF INVENTION: VIRUSES, AND USES THEREOF

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 SOUTH JEFFERSON5Xe S HIGHWAY, FOURTH ho n

; STREET: FLOOR

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,410

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/894,699

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,614

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-40

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||
Db 4 RARLLA 9

RESULT 12

US-09-444-410-68

; Sequence 68, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-68

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||
Db 4 RARLLA 9

RESULT 13

US-09-041-886-37

; Sequence 37, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-37

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
|||||
Db 21 LLAAL 25

RESULT 14

US-09-041-886-38

; Sequence 38, Application US/09041886
; Patent No. 6235872

; GENERAL INFORMATION:

; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-041-886-38

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 21 LLAAL 25

RESULT 15

US-09-041-886-39

; Sequence 39, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-39

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 21 LLAAL 25

RESULT 16

US-09-041-886-40
; Sequence 40, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-40

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 21 LLAAL 25

RESULT 17

US-09-041-886-54
; Sequence 54, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence

; TITLE OF INVENTION: Polypeptides and Methods of Use
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/041,886
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 2626
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-041-886-54

Query Match 12.8%; Score 5; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 21 LLAAL 25

RESULT 18
 US-09-205-258-614
 ; Sequence 614, Application US/09205258
 ; Patent No. 6525174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: PZ007P1
 ; CURRENT APPLICATION NUMBER: US/09/205,258
 ; CURRENT FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 614
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-614
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Query Match          12.8%; Score 5; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Qy          7 DAAFR 11
            |||||
Db          13 DAAFR 17
```

RESULT 19

US-08-786-284A-3

```
; Sequence 3, Application US/08786284A
; Patent No. 6273598
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: GRIFFITH, DIANA L
; APPLICANT: CARLSON, WILLIAM D
; APPLICANT: RUEGER, DAVID C
; APPLICANT: SAMPATH, KUBER T
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
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```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,284A
; FILING DATE:
; CLASSIFICATION: 364
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-0992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..32
; OTHER INFORMATION: /product= "PEPTIDE H-1"
US-08-786-284A-3

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Query Match          12.8%; Score 5; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      26 LNSYM 30
        |||||
Db      5 LNSYM 9

```

RESULT 20

```

US-08-704-856C-3
; Sequence 3, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
US-08-704-856C-3

```

```

Query Match          12.8%; Score 5; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      3 ALADD 7
        |||||
Db      29 ALADD 33

```

```

RESULT 21
US-09-242-881-3
; Sequence 3, Application US/09242881
; Patent No. 6448070
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
;            Yusibov, Vidadi
;            Hooper, Douglas, C.
;            Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
;                    Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-242-881-3

```

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Query Match          12.8%; Score 5; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 ALADD 7
        |||||
Db      29 ALADD 33

```

```

RESULT 22
5514590-5
;Patent No. 5514590
; APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.;JAMES, ERIC
; TITLE OF INVENTION: EXPRESSION SYSTEM COMPRISING DNA
;ENCODING THE SIGNAL PEPTIDE OF PROTEASE B FROM STREPTOMYCES
;GRISEUS
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,644
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 66,938
; FILING DATE: 25-MAY-1993
; APPLICATION NUMBER: 844,937
; FILING DATE: 04-MAR-1992
; APPLICATION NUMBER: 221,346
; FILING DATE: 18-JUL-1988
; APPLICATION NUMBER: 795,331
; FILING DATE: 06-NOV-1985
;SEQ ID NO:5:
; LENGTH: 38
5514590-5

```

```

Query Match          12.8%; Score 5; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ARLLA 18
|||||
Db 16 ARLLA 20

RESULT 23

US-09-406-045-11

; Sequence 11, Application US/09406045
; Patent No. 6451994
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 23413, A NOVEL HUMAN UBIQUITIN
; FILE REFERENCE: 5800-50
; CURRENT APPLICATION NUMBER: US/09/406,045
; CURRENT FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ProDom consensus sequence
US-09-406-045-11

Query Match 12.8%; Score 5; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LERRH 24
|||||
Db 15 LERRH 19

RESULT 24

US-07-690-300B-44

; Sequence 44, Application US/07690300B
; Patent No. 5234907
; GENERAL INFORMATION:
; APPLICANT: Bolin, David R.
; TITLE OF INVENTION: Synthetic Vasoactive Intestinal Peptide
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/690,300B
; FILING DATE: 19910424
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/374,503
; FILING DATE: 30-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokras, Bruce A.
; REGISTRATION NUMBER: 32,748
; REFERENCE/DOCKET NUMBER: 8480
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-5801
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 17
; OTHER INFORMATION: /note= "Xaa=Nle"
US-07-690-300B-44

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 DAAF 10
        ||||
Db      3 DAAF 6

```

RESULT 25

US-07-789-344A-11

```

; Sequence 11, Application US/07789344A
; Patent No. 5318897
; GENERAL INFORMATION:
; APPLICANT: Sudhir, Paul
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ANTIBODY
; TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN
; TITLE OF INVENTION: GROUND STATE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,344A
; FILING DATE: 08-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-789-344A-11

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      25 WLNS 28
        |||
Db      22 WLNS 25

```

RESULT 26

US-07-728-221B-3

; Sequence 3, Application US/07728221B

; Patent No. 5340920

; GENERAL INFORMATION:

; APPLICANT: Matsuo, Hisayuki

; APPLICANT: Kangawa, Kenji

; APPLICANT: Minamino, Naoto

; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE

; TITLE OF INVENTION: PEPTIDE (CNP-53)

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/07/728,221B
; FILING DATE: 19910712
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 671 4627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-728-221B-3

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      14 ARL 17
        |||
Db      10 ARL 13

```

RESULT 27

US-08-276-852-13

```

; Sequence 13, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994

```

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-852-13

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      16 LLAA 19
        ||||
Db      14 LLAA 17

```

RESULT 28

```

US-08-664-449-37
; Sequence 37, Application US/08664449
; Patent No. 5766905
; GENERAL INFORMATION:
; APPLICANT: Studier, F. W.
; APPLICANT: Rosenberg, Alan H.
; TITLE OF INVENTION: Cytoplasmic Bacteriophage Display System
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET: Building 902C
; CITY: Upton
; STATE: NY
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,449
; FILING DATE: 17-June-1996
; CLASSIFICATION: 435

```



```

; ATTORNEY/AGENT INFORMATION:
;   NAME:  Bogosian, Margaret
;   REGISTRATION NUMBER:  25,324
;   REFERENCE/DOCKET NUMBER:  AUI-9618
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (516) 344-7338
;   TELEFAX:  (516) 344-3729
; INFORMATION FOR SEQ ID NO:  37:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  28 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-664-449-37

```

```

Query Match          10.3%;  Score 4;  DB 1;  Length 28;
Best Local Similarity 100.0%;  Pred. No. 2.6e+03;
Matches      4;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      18 AALE 21
        ||||
Db      25 AALE 28

```

RESULT 29

US-08-899-575-13

```

; Sequence 13, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
;   APPLICANT:  Burton, Dennis R
;   APPLICANT:  Barbas, Carlos F
;   APPLICANT:  Lerner, Richard A
;   TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;   NUMBER OF SEQUENCES:  170
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  The Scripps Research Institute, Office of
;     ADDRESSEE:  Patent Counsel
;     STREET:  10666 No. 5770440th Torrey Pines Road, Suite 220,
;     STREET:  Mail Drop TPC8
;     CITY:  La Jolla
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/899,575
;     FILING DATE:  24-JUL-1997
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/276,852
;     FILING DATE:  18-JUL-1994
;     APPLICATION NUMBER:  US 08/178,302

```

```

; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-899-575-13

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      16 LLAA 19
        ||||
Db      14 LLAA 17

```

RESULT 30

US-08-899-575-13

```

; Sequence 13, Application US/08899575
; Patent No. 5804440

```

GENERAL INFORMATION:

```

; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

```

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-899-575-13

```

```

Query Match          10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      16 LLAA 19
        ||||
Db      14 LLAA 17

```

RESULT 31

US-08-458-568A-6

```

; Sequence 6, Application US/08458568A
; Patent No. 5821339
; GENERAL INFORMATION:
; APPLICANT: Schaffer, Priscilla A.
; APPLICANT: Yeh, Lily
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
; TITLE OF INVENTION: Infections
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPer2263.1;
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-568A-6

```

```

Query Match          10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 RERA 14
        ||||
Db      10 RERA 13

```

RESULT 32

US-08-788-231A-18

```

; Sequence 18, Application US/08788231A
; Patent No. 6019974
; GENERAL INFORMATION:
; APPLICANT: L'Hernault, Steven W.
; TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,231A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 60/010,672
 ; FILING DATE: 26-JAN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferber, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER: 60-95
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: YES
 US-08-788-231A-18

Query Match 10.3%; Score 4; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLVL 36
 ||||
 Db 19 LLVL 22

RESULT 33

US-09-348-578-3

; Sequence 3, Application US/09348578
 ; Patent No. 6160089
 ; GENERAL INFORMATION:
 ; APPLICANT: HONJO, Masaru
 ; APPLICANT: NAITOH, Naokazu
 ; APPLICANT: UCHIDA, Hiroshi
 ; APPLICANT: MOCHIZUKI, Daisuke
 ; APPLICANT: MATSUMOTO, Kazuya
 ; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
 ; FILE REFERENCE: 029430-421
 ; CURRENT APPLICATION NUMBER: US/09/348,578
 ; CURRENT FILING DATE: 1999-07-07
 ; EARLIER APPLICATION NUMBER: JP 193003/1998
 ; EARLIER FILING DATE: 1998-07-08
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
 secretion
 ; OTHER INFORMATION: signal
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)..(28)

US-09-348-578-3

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 17 LAAL 20

RESULT 34

US-09-348-578-11

; Sequence 11, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
secretion
; OTHER INFORMATION: signal
US-09-348-578-11

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 17 LAAL 20

RESULT 35

US-09-348-578-19

; Sequence 19, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru

```

; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
secretion
; OTHER INFORMATION: signal
US-09-348-578-19

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Query Match          10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      17 LAAL 20
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Db      17 LAAL 20

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RESULT 36

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US-08-974-549A-166
; Sequence 166, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/974,549A
;     FILING DATE:  19-NOV-1997
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/724,643
;     FILING DATE:  01-OCT-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/844,419
;     FILING DATE:  18-APR-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/846,017
;     FILING DATE:  25-APR-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/851,843
;     FILING DATE:  06-MAY-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/854,050
;     FILING DATE:  09-MAY-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/911,312
;     FILING DATE:  14-AUG-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/912,951
;     FILING DATE:  14-AUG-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/915,503
;     FILING DATE:  14-AUG-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO PCT/US97/17618
;     FILING DATE:  01-OCT-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO PCT/US97/17885
;     FILING DATE:  01-OCT-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Apple, Randolph Ted
;     REGISTRATION NUMBER:  36,429
;     REFERENCE/DOCKET NUMBER:  015389-002610US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 576-0200
;     TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 166:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-974-549A-166

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Query Match          10.3%;  Score 4;  DB 3;  Length 28;
Best Local Similarity 100.0%;  Pred. No. 2.6e+03;
Matches      4;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy 26 LNSY 29
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Db 7 LNSY 10

RESULT 37

US-09-107-991-12

; Sequence 12, Application US/09107991
; Patent No. 6221626
; GENERAL INFORMATION:
; APPLICANT: Bienvenut, Willy V.
; APPLICANT: Hochstrasser, Denis F.
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112-0028
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,991
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K. Ph.D.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A31855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)705-5000
; TELEFAX: (212)705-5020
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-107-991-12

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ARLL 17
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Db 14 ARLL 17

RESULT 38

US-09-041-886-42
; Sequence 42, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-42

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
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Db 22 LAAL 25

RESULT 39

US-09-507-819-30
; Sequence 30, Application US/09507819
; Patent No. 6303314
; GENERAL INFORMATION:
; APPLICANT: Jingwu, Zhang Z.
; TITLE OF INVENTION: T Cell Receptor VB-D8A7B Sequen64;25X0
; Patent No. 6303314

s For Its

; TITLE OF INVENTION: Detection
; FILE REFERENCE: BCOL003
; CURRENT APPLICATION NUMBER: US/09/507,819
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-507-819-30

Query Match 10.3%; Score 4; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
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Db 20 LLVL 23

RESULT 40

US-09-099-041A-19
; Sequence 19, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-19

Query Match 10.3%; Score 4; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
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Db 22 LALA 25

Search completed: January 14, 2004, 10:43:44
Job time : 18.243 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 11.5421 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	12.8	29	2	G83440	KdpF protein PA163
2	5	12.8	29	2	A32860	biotin-binding pro
3	5	12.8	31	2	S05124	hypothetical prote
4	5	12.8	31	2	S58569	hypothetical prote
5	5	12.8	31	2	T14568	hypothetical prote
6	5	12.8	33	2	A82451	hypothetical prote
7	5	12.8	38	2	G97576	hypothetical prote
8	4	10.3	28	2	T14210	NADH2 dehydrogenas
9	4	10.3	28	2	S21278	glutathione transf
10	4	10.3	28	2	B35948	phospholipase A2 (
11	4	10.3	28	2	A56366	intestinal trefoil
12	4	10.3	28	2	PH0231	T-cell receptor Vb
13	4	10.3	28	2	T06925	hypothetical prote

14	4	10.3	28	2	JQ1035	hypothetical 3.2K
15	4	10.3	29	2	E47719	house-dust-mite-re
16	4	10.3	29	2	S58390	T-cell receptor be
17	4	10.3	29	2	I37534	gene HLA-DRB prote
18	4	10.3	29	2	I37535	gene HLA-DRB prote
19	4	10.3	29	2	I37536	MHC class II histo
20	4	10.3	29	2	I37301	MHC class II histo
21	4	10.3	29	2	I37303	HLA-DR beta - huma
22	4	10.3	29	2	I37306	HLA-DR beta - huma
23	4	10.3	29	2	S78326	conserved hypothet
24	4	10.3	29	2	S16323	hypothetical prote
25	4	10.3	29	2	S78714	protein YDR524w-a
26	4	10.3	30	2	S21195	spectrin beta chai
27	4	10.3	30	2	S30333	N-carbamoyl-D-amin
28	4	10.3	30	2	E84786	hypothetical prote
29	4	10.3	31	2	PH0236	T-cell receptor Vb
30	4	10.3	31	2	I48082	mitochondrial benz
31	4	10.3	31	2	S76281	hypothetical prote
32	4	10.3	31	2	S74965	photosystem I reac
33	4	10.3	31	2	D82827	hypothetical prote
34	4	10.3	31	2	T07290	photosystem I prot
35	4	10.3	32	2	D61014	defensin NP-1 - ra
36	4	10.3	32	2	E61014	defensin R-5 - rat
37	4	10.3	32	2	A25735	interphotoreceptor
38	4	10.3	32	2	C84355	hypothetical prote
39	4	10.3	32	2	PC7067	meltrin beta - mou
40	4	10.3	33	2	A44181	Cerastes serine pr
41	4	10.3	33	2	B56635	tubulin alpha chai
42	4	10.3	33	2	A05010	hypothetical prote
43	4	10.3	33	2	H95094	hypothetical prote
44	4	10.3	33	2	PC7035	reversion inducing
45	4	10.3	33	2	E45557	orf immediately up
46	4	10.3	33	2	A82288	hypothetical prote
47	4	10.3	33	2	F97371	hypothetical prote
48	4	10.3	34	2	S71457	NADH2 dehydrogenas
49	4	10.3	34	2	C56635	tubulin alpha chai
50	4	10.3	34	2	A84391	hypothetical prote
51	4	10.3	35	2	A05112	M24 protein - Stre
52	4	10.3	35	2	S65772	early nodulin 40 -
53	4	10.3	35	2	A81346	hypothetical prote
54	4	10.3	35	2	D97553	hypothetical prote
55	4	10.3	35	2	AI1823	photosystem II Psb
56	4	10.3	36	2	S70806	hypothetical prote
57	4	10.3	36	2	D87544	hypothetical prote
58	4	10.3	36	2	E70238	hypothetical prote
59	4	10.3	36	2	A41017	LDL receptor-relat
60	4	10.3	36	2	A61316	largomycin - Strep
61	4	10.3	37	2	C45187	homeotic protein G
62	4	10.3	37	2	C84210	hypothetical prote
63	4	10.3	37	2	H72308	hypothetical prote
64	4	10.3	37	2	F82102	hypothetical prote
65	4	10.3	37	2	A57127	diuretic hormone 1
66	4	10.3	37	2	H83756	hypothetical prote
67	4	10.3	37	2	JC6153	viral capsid prote
68	4	10.3	38	2	T11763	acetyl-CoA carboxy
69	4	10.3	38	2	B82413	hypothetical prote
70	4	10.3	38	2	T34678	hypothetical prote

71	4	10.3	38	2	E37334	alcohol dehydrogen
72	4	10.3	39	2	S51003	hypothetical prote
73	4	10.3	39	2	B87458	hypothetical prote
74	4	10.3	39	2	B82452	hypothetical prote
75	4	10.3	39	2	E69677	phosphatase (RapI)
76	4	10.3	39	2	F82767	hypothetical prote
77	4	10.3	39	2	C85911	hypothetical prote
78	4	10.3	40	2	S39822	hypothetical prote
79	4	10.3	40	2	S43028	ribosomal protein
80	4	10.3	40	2	A64530	hypothetical prote
81	4	10.3	40	2	D83378	hypothetical prote
82	4	10.3	40	2	S01102	hypothetical prote
83	3	7.7	28	2	S71598	cytochrome P450 HP
84	3	7.7	28	2	S04341	cytochrome P450 PB
85	3	7.7	28	2	PX0033	cytochrome P450 te
86	3	7.7	28	2	S66436	allophycocyanin al
87	3	7.7	28	2	T12301	NADH2 dehydrogenas
88	3	7.7	28	2	A34244	hexokinase (EC 2.7
89	3	7.7	28	2	A31859	deoxycytidine kina
90	3	7.7	28	2	A38296	sterol esterase (E
91	3	7.7	28	2	A35115	hypothetical prote
92	3	7.7	28	2	S55729	orotidine-5'-monop
93	3	7.7	28	2	A61322	somatostatin-28 -
94	3	7.7	28	2	B60071	vasoactive intesti
95	3	7.7	28	2	A60304	vasoactive intesti
96	3	7.7	28	2	A38232	vasoactive intesti
97	3	7.7	28	2	A60303	vasoactive intesti
98	3	7.7	28	2	JT0412	bombyxin-IV chain
99	3	7.7	28	2	A49829	T-cell receptor va
100	3	7.7	28	2	S11618	ribosomal protein
101	3	7.7	28	2	I50169	alpha-1 type-1 col
102	3	7.7	28	2	S55442	beta A2 crystallin
103	3	7.7	28	2	I48349	fibronectin - mous
104	3	7.7	28	2	F54346	pyruvate synthase
105	3	7.7	28	2	S29135	aminopyrine N-deme
106	3	7.7	28	2	S29136	aminopyrine N-deme
107	3	7.7	28	2	PN0625	homeobox JRX prote
108	3	7.7	28	2	B56779	tetM 5'-region lea
109	3	7.7	28	2	B47310	MHVS28AA - murine
110	3	7.7	28	2	S15235	hypothetical prote
111	3	7.7	28	2	I60364	phosphorybosylpyro
112	3	7.7	28	2	S70894	hypothetical prote
113	3	7.7	28	2	B39191	hypothetical prote
114	3	7.7	28	2	S63502	95K protein - Euba
115	3	7.7	28	2	T14905	hypothetical prote
116	3	7.7	28	2	JQ0272	hypothetical 3K pr
117	3	7.7	28	2	A44923	carboxypeptidase 3
118	3	7.7	28	2	A60698	trichocyst protein
119	3	7.7	28	2	A27261	proteinase inhibit
120	3	7.7	28	2	I59477	antigen, T-cell re
121	3	7.7	28	2	S54338	cytochrome P450 CY
122	3	7.7	28	2	I52627	erythrocyte chemok
123	3	7.7	28	2	PH1335	Ig heavy chain DJ
124	3	7.7	28	2	PT0366	T-cell receptor be
125	3	7.7	28	2	I58115	cystic fibrosis tr
126	3	7.7	28	2	B83797	hypothetical prote
127	3	7.7	28	2	C83797	hypothetical prote

128	3	7.7	28	2	C83969	hypothetical prote
129	3	7.7	28	2	S51593	myrB protein - Mic
130	3	7.7	28	2	H85908	hypothetical prote
131	3	7.7	28	4	JN0014	GABA(A) receptor a
132	3	7.7	29	1	Q1BP57	gene 1.5 protein -
133	3	7.7	29	2	A60558	cytochrome P450 HL
134	3	7.7	29	2	A48427	flavoheemoglobin hm
135	3	7.7	29	2	PC2364	protoporphyrinogen
136	3	7.7	29	2	S08201	peroxidase (EC 1.1
137	3	7.7	29	2	S39968	probable hydro-lya
138	3	7.7	29	2	S28174	heat-shock protein
139	3	7.7	29	2	S17432	H+-transporting tw
140	3	7.7	29	2	T03653	phospholipid trans
141	3	7.7	29	2	A39462	cholestinin - do
142	3	7.7	29	2	S17147	galanin - chicken
143	3	7.7	29	2	I52628	low affinity nerve
144	3	7.7	29	2	C61233	conceptus protein
145	3	7.7	29	2	C47719	T-cell receptor al
146	3	7.7	29	2	S10050	ribosomal protein
147	3	7.7	29	2	S26229	ribosomal protein
148	3	7.7	29	2	S10725	calmodulin-binding
149	3	7.7	29	2	S57232	homeotic protein s
150	3	7.7	29	2	T51116	probable precorrin
151	3	7.7	29	2	B34490	lens fiber cell me
152	3	7.7	29	2	A35121	hypothetical prote
153	3	7.7	29	2	G90719	hypothetical prote
154	3	7.7	29	2	S14040	hypothetical prote
155	3	7.7	29	2	G64674	hypothetical prote
156	3	7.7	29	2	T48910	KdpF protein [vali
157	3	7.7	29	2	S65747	CDP-paratose synth
158	3	7.7	29	2	S65748	CDP-paratose synth
159	3	7.7	29	2	S05224	photosystem I 4.8K
160	3	7.7	29	2	S74572	hypothetical prote
161	3	7.7	29	2	S67989	HA-19/HA-52 protei
162	3	7.7	29	2	S77569	plantaricin SA6 -
163	3	7.7	29	2	B41476	probable antigen 2
164	3	7.7	29	2	S03947	hydrogen dehydroge
165	3	7.7	29	2	T37120	hypothetical prote
166	3	7.7	29	2	T36654	probable small mem
167	3	7.7	29	2	B43937	endo-1,4-beta-xyla
168	3	7.7	29	2	T06904	hypothetical prote
169	3	7.7	29	2	S73197	hypothetical prote
170	3	7.7	29	2	S78360	hypothetical prote
171	3	7.7	29	2	S01572	hypothetical prote
172	3	7.7	29	2	T07450	hypothetical prote
173	3	7.7	29	2	S01448	hypothetical prote
174	3	7.7	29	2	S43992	peroxidase (EC 1.1
175	3	7.7	29	2	JQ0212	hypothetical 3K pr
176	3	7.7	29	2	S58541	hypothetical prote
177	3	7.7	29	2	S68094	2,3-dihydroxybenzo
178	3	7.7	29	2	B21112	variant surface gl
179	3	7.7	29	2	B60698	trichocyst protein
180	3	7.7	29	2	A61613	ceratotoxin A - Me
181	3	7.7	29	2	B61613	ceratotoxin B - Me
182	3	7.7	29	2	I50695	non-collagenous al
183	3	7.7	29	2	I77372	CD44SP - human
184	3	7.7	29	2	C54037	splicing regulator

185	3	7.7	29	2	S57204	oviduct-specific s
186	3	7.7	29	2	S38749	vimentin homolog -
187	3	7.7	29	2	A83923	hypothetical prote
188	3	7.7	29	2	B85840	hypothetical prote
189	3	7.7	29	2	C85840	hypothetical prote
190	3	7.7	29	2	AH2338	PetN protein [impo
191	3	7.7	30	1	TIPU1W	trypsin inhibitor
192	3	7.7	30	1	CLHRY2	protamine YII - Pa
193	3	7.7	30	1	CLHR2A	protamine YII - At
194	3	7.7	30	2	I57689	ubiquinol-cytochro
195	3	7.7	30	2	PQ0723	parvalbumin [impor
196	3	7.7	30	2	S08202	peroxidase (EC 1.1
197	3	7.7	30	2	S08204	peroxidase (EC 1.1
198	3	7.7	30	2	S08203	peroxidase (EC 1.1
199	3	7.7	30	2	C21897	ornithine carbamoy
200	3	7.7	30	2	A28562	glutathione transf
201	3	7.7	30	2	A27103	aspartate transami
202	3	7.7	30	2	I55427	aspartate transami
203	3	7.7	30	2	S68639	nigroxin A - black
204	3	7.7	30	2	S68640	nigroxin B - black
205	3	7.7	30	2	PX0073	epoxide hydrolase
206	3	7.7	30	2	A61333	trypsin (EC 3.4.21
207	3	7.7	30	2	S60893	InvC protein - Sal
208	3	7.7	30	2	S24979	proteinase inhibit
209	3	7.7	30	2	JX0057	trypsin inhibitor
210	3	7.7	30	2	A61130	somatotropin - Ame
211	3	7.7	30	2	A59076	defensin alpha-1 -
212	3	7.7	30	2	B59076	defensin alpha-2 -
213	3	7.7	30	2	C59076	defensin alpha-3 -
214	3	7.7	30	2	I68109	interferon alpha-W
215	3	7.7	30	2	PH0237	T-cell receptor Vb
216	3	7.7	30	2	PH0882	Ig kappa chain V r
217	3	7.7	30	2	A21680	hemoglobin epsilon
218	3	7.7	30	2	A05254	hemoglobin epsilon
219	3	7.7	30	2	S07217	ribosomal protein
220	3	7.7	30	2	I52806	Duchenne muscular
221	3	7.7	30	2	B61511	serum albumin, mil
222	3	7.7	30	2	S57234	fushi tarazu segme
223	3	7.7	30	2	S07065	rRNA N-glycosidase
224	3	7.7	30	2	A31836	17K antigen - Rick
225	3	7.7	30	2	A22977	delta-endotoxin -
226	3	7.7	30	2	A44913	34K core flagella
227	3	7.7	30	2	S08565	ribulose-bisphosph
228	3	7.7	30	2	S30757	genome polyprotein
229	3	7.7	30	2	S30759	genome polyprotein
230	3	7.7	30	2	B44314	intracisternal A p
231	3	7.7	30	2	I58367	gag protein - mous
232	3	7.7	30	2	S42364	aromatic-amino-aci
233	3	7.7	30	2	PS0437	potassium channel
234	3	7.7	30	2	PQ0444	hypothetical prote
235	3	7.7	30	2	C95030	hypothetical prote
236	3	7.7	30	2	F95118	hypothetical prote
237	3	7.7	30	2	A84412	hypothetical prote
238	3	7.7	30	2	S15141	hypothetical prote
239	3	7.7	30	2	D72276	hypothetical prote
240	3	7.7	30	2	E72356	hypothetical prote
241	3	7.7	30	2	H72312	hypothetical prote

242	3	7.7	30	2	D70253	conserved hypothet
243	3	7.7	30	2	H70152	hypothetical prote
244	3	7.7	30	2	B70165	hypothetical prote
245	3	7.7	30	2	A70209	hypothetical prote
246	3	7.7	30	2	H64522	hypothetical prote
247	3	7.7	30	2	S14365	4-sulfobenzoate 3,
248	3	7.7	30	2	A83556	hypothetical prote
249	3	7.7	30	2	S30347	4-hydroxybenzoyl-C
250	3	7.7	30	2	B81889	hypothetical prote
251	3	7.7	30	2	A36733	hypothetical prote
252	3	7.7	30	2	C82341	hypothetical prote
253	3	7.7	30	2	A82137	hypothetical prote
254	3	7.7	30	2	C82092	hypothetical prote
255	3	7.7	30	2	H82510	hypothetical prote
256	3	7.7	30	2	B82428	hypothetical prote
257	3	7.7	30	2	S78303	photosystem I prot
258	3	7.7	30	2	S19609	glucoooligosacchari
259	3	7.7	30	2	D32946	serine proteinase
260	3	7.7	30	2	B60914	pheromone-binding
261	3	7.7	30	2	A61546	beta-N-acetylgluco
262	3	7.7	30	2	S23365	T-cell receptor al
263	3	7.7	30	2	B46958	androgen-binding p
264	3	7.7	30	2	S48114	cystic fibrosis tr
265	3	7.7	30	2	B84053	hypothetical prote
266	3	7.7	30	2	C71309	hypothetical prote
267	3	7.7	30	2	G82515	hypothetical prote
268	3	7.7	30	2	A48923	retrovirus-related
269	3	7.7	30	2	E85694	hypothetical prote
270	3	7.7	30	2	F89864	hypothetical prote
271	3	7.7	30	2	S34761	L-serine ammonia-l
272	3	7.7	31	1	CLHRZ	protamine Z - Paci
273	3	7.7	31	1	CLHRZA	protamine Z - Atla
274	3	7.7	31	1	JU0351	3.6K protein - Chl
275	3	7.7	31	1	D64117	ftsH protein homol
276	3	7.7	31	1	S34504	photosystem I prot
277	3	7.7	31	2	S13205	glyceraldehyde-3-p
278	3	7.7	31	2	S18356	chymotrypsin (EC 3
279	3	7.7	31	2	S61558	chymotrypsin Pml -
280	3	7.7	31	2	PC1269	subtilisin inhibit
281	3	7.7	31	2	S21743	trypsin inhibitor
282	3	7.7	31	2	S39019	glucagon-like pept
283	3	7.7	31	2	F30608	Ig kappa chain V-I
284	3	7.7	31	2	D30608	Ig kappa chain V-I
285	3	7.7	31	2	E53480	T-cell receptor al
286	3	7.7	31	2	S03297	Ig alpha chain C r
287	3	7.7	31	2	A34448	myosin heavy chain
288	3	7.7	31	2	A20883	variant surface gl
289	3	7.7	31	2	I39679	exeE protein - Aer
290	3	7.7	31	2	S03336	photosystem II pro
291	3	7.7	31	2	B41453	translation elonga
292	3	7.7	31	2	S53132	gene X protein - h
293	3	7.7	31	2	S53135	gene X protein - h
294	3	7.7	31	2	S53138	gene X protein - h
295	3	7.7	31	2	S53141	gene X protein - h
296	3	7.7	31	2	S53147	gene X protein - h
297	3	7.7	31	2	S53150	gene X protein - h
298	3	7.7	31	2	S53153	gene X protein - h

299	3	7.7	31	2	S53156	gene X protein - h
300	3	7.7	31	2	S53160	gene X protein - h
301	3	7.7	31	2	S53162	gene X protein - h
302	3	7.7	31	2	S53164	gene X protein - h
303	3	7.7	31	2	S53176	gene X protein - h
304	3	7.7	31	2	S53179	gene X protein - h
305	3	7.7	31	2	S53187	gene X protein - h
306	3	7.7	31	2	S53190	gene X protein - h
307	3	7.7	31	2	S53192	gene X protein - h
308	3	7.7	31	2	S53199	gene X protein - h
309	3	7.7	31	2	S53201	gene X protein - h
310	3	7.7	31	2	S53205	gene X protein - h
311	3	7.7	31	2	S53208	gene X protein - h
312	3	7.7	31	2	S53215	gene X protein - h
313	3	7.7	31	2	S53219	gene X protein - h
314	3	7.7	31	2	S53228	gene X protein - h
315	3	7.7	31	2	S53254	gene X protein - h
316	3	7.7	31	2	S53258	gene X protein - h
317	3	7.7	31	2	S53282	gene X protein - h
318	3	7.7	31	2	S53284	gene X protein - h
319	3	7.7	31	2	S53287	gene X protein - h
320	3	7.7	31	2	S53289	gene X protein - h
321	3	7.7	31	2	D34490	lens fiber cell me
322	3	7.7	31	2	T36124	hypothetical prote
323	3	7.7	31	2	S65418	pyruvate synthase
324	3	7.7	31	2	C54346	pyruvate synthase
325	3	7.7	31	2	A23341	allergen R7 - pere
326	3	7.7	31	2	C95010	hypothetical prote
327	3	7.7	31	2	G95022	hypothetical prote
328	3	7.7	31	2	A95237	hypothetical prote
329	3	7.7	31	2	H72808	gp82.2 protein - M
330	3	7.7	31	2	S40665	hypothetical prote
331	3	7.7	31	2	C48472	capsid protein VP-
332	3	7.7	31	2	F72270	hypothetical prote
333	3	7.7	31	2	E70223	hypothetical prote
334	3	7.7	31	2	C71845	hypothetical prote
335	3	7.7	31	2	B81027	lacto-N-neotetraos
336	3	7.7	31	2	T08489	hypothetical prote
337	3	7.7	31	2	C82175	hypothetical prote
338	3	7.7	31	2	B82138	hypothetical prote
339	3	7.7	31	2	G82071	hypothetical prote
340	3	7.7	31	2	G82066	hypothetical prote
341	3	7.7	31	2	E82466	hypothetical prote
342	3	7.7	31	2	S31075	hypothetical prote
343	3	7.7	31	2	S16049	photosystem I prot
344	3	7.7	31	2	T46840	hypothetical prote
345	3	7.7	31	2	T36103	hypothetical prote
346	3	7.7	31	2	T36022	small hypothetical
347	3	7.7	31	2	T06934	photosystem I chai
348	3	7.7	31	2	T06854	photosystem II pro
349	3	7.7	31	2	S73244	photosystem II pro
350	3	7.7	31	2	S78335	hypothetical prote
351	3	7.7	31	2	A53841	ycf8 protein - Eug
352	3	7.7	31	2	S20491	hypothetical prote
353	3	7.7	31	2	A05051	hypothetical prote
354	3	7.7	31	2	B20883	variant surface gl
355	3	7.7	31	2	T16215	hypothetical prote

356	3	7.7	31	2	G24802	cuticle protein 54
357	3	7.7	31	2	B60363	apolipophorin III
358	3	7.7	31	2	B42176	insulin-like growt
359	3	7.7	31	2	I61697	myosin - human (fr
360	3	7.7	31	2	I46598	myosin - pig (frag
361	3	7.7	31	2	I46276	hemoglobin beta-x
362	3	7.7	31	2	S27112	sarcolipin - rabbi
363	3	7.7	31	2	T09121	hypothetical prote
364	3	7.7	31	2	G82766	hypothetical prote
365	3	7.7	31	2	C82620	hypothetical prote
366	3	7.7	31	2	T07276	photosystem II pro
367	3	7.7	31	2	B85582	unknown protein en
368	3	7.7	31	2	AB0049	transposase (parti
369	3	7.7	31	2	AD2046	hypothetical prote
370	3	7.7	32	1	TCEE	calcitonin - Japan
371	3	7.7	32	1	TCON2	calcitonin 2 - soc
372	3	7.7	32	1	TCON2C	calcitonin 2 - chu
373	3	7.7	32	1	TCON2P	calcitonin 2 - pin
374	3	7.7	32	1	TCON3	calcitonin 3 - coh
375	3	7.7	32	1	IRTR2	protamine II - rai
376	3	7.7	32	1	LFECI	ilvGMEDA operon le
377	3	7.7	32	1	LFEBIT	ilvGEDA leader pep
378	3	7.7	32	1	LFECIV	ilvBN operon leade
379	3	7.7	32	2	JT0017	ferredoxin [2Fe-2S
380	3	7.7	32	2	S20719	alcohol dehydrogen
381	3	7.7	32	2	A56672	methylguanidine-sy
382	3	7.7	32	2	S35583	glutathione transf
383	3	7.7	32	2	G46376	1-aminocyclopropan
384	3	7.7	32	2	A32502	T-cell receptor de
385	3	7.7	32	2	E60505	hemoglobin A2-3 be
386	3	7.7	32	2	S05455	histone H2A - brin
387	3	7.7	32	2	I51089	protamine - Japane
388	3	7.7	32	2	A02687	DNA-binding protei
389	3	7.7	32	2	S51061	ribosomal protein
390	3	7.7	32	2	A24047	gap junction prote
391	3	7.7	32	2	S72220	alpha-S1-casein -
392	3	7.7	32	2	S36809	GTP-binding regula
393	3	7.7	32	2	A61052	heat shock protein
394	3	7.7	32	2	I48415	heat shock factor
395	3	7.7	32	2	A59156	gliadin omega-5 -
396	3	7.7	32	2	E91216	ilvGEDA operon lea
397	3	7.7	32	2	F86062	ilvGMEDA operon le
398	3	7.7	32	2	AG0924	ilvGMEDA operon at
399	3	7.7	32	2	E91205	ilvB operon leader
400	3	7.7	32	2	G86051	ilvBN operon leade
401	3	7.7	32	2	A44906	L1 protein - human
402	3	7.7	32	2	S19906	E6-II protein - hu
403	3	7.7	32	2	PQ0425	nonstructural prot
404	3	7.7	32	2	PQ0413	nonstructural prot
405	3	7.7	32	2	PQ0419	nonstructural prot
406	3	7.7	32	2	C58493	group I allergen A
407	3	7.7	32	2	B58493	group I allergen A
408	3	7.7	32	2	S03273	photosystem II oxy
409	3	7.7	32	2	C46107	polyomavirus enhan
410	3	7.7	32	2	S57228	zen protein (clone
411	3	7.7	32	2	A95108	hypothetical prote
412	3	7.7	32	2	A95137	hypothetical prote

413	3	7.7	32	2	G95225	hypothetical prote
414	3	7.7	32	2	E87701	hypothetical prote
415	3	7.7	32	2	G84161	hypothetical prote
416	3	7.7	32	2	H70153	hypothetical prote
417	3	7.7	32	2	D70222	hypothetical prote
418	3	7.7	32	2	E70225	hypothetical prote
419	3	7.7	32	2	G70249	hypothetical prote
420	3	7.7	32	2	B70257	hypothetical prote
421	3	7.7	32	2	D55230	phosphoenolpyruvat
422	3	7.7	32	2	E82279	hypothetical prote
423	3	7.7	32	2	F82097	hypothetical prote
424	3	7.7	32	2	C82467	hypothetical prote
425	3	7.7	32	2	B82421	hypothetical prote
426	3	7.7	32	2	H82416	hypothetical prote
427	3	7.7	32	2	F82407	hypothetical prote
428	3	7.7	32	2	S23476	hypothetical prote
429	3	7.7	32	2	S07713	hypothetical prote
430	3	7.7	32	2	S22304	hypothetical prote
431	3	7.7	32	2	T36275	hypothetical prote
432	3	7.7	32	2	S73196	hypothetical prote
433	3	7.7	32	2	S78323	photosystem II pro
434	3	7.7	32	2	A05015	hypothetical prote
435	3	7.7	32	2	B38578	protein kinase 1 (
436	3	7.7	32	2	S35053	L-mandelate dehydr
437	3	7.7	32	2	S36825	UDP-galactose-N-ac
438	3	7.7	32	2	A61624	apolipoprotein-III
439	3	7.7	32	2	F82833	hypothetical prote
440	3	7.7	32	2	E85588	hypothetical prote
441	3	7.7	32	2	S78776	imelysin (EC 3.4.2
442	3	7.7	32	2	AB0774	hypothetical prote
443	3	7.7	33	1	A23483	alcohol oxidase (E
444	3	7.7	33	1	WRECP1	protamine-like pro
445	3	7.7	33	1	FDFI5G	antifreeze protein
446	3	7.7	33	2	A36154	benzphetamine N-de
447	3	7.7	33	2	JT0022	ferredoxin [2Fe-2S
448	3	7.7	33	2	B60743	ornithine carbamoy
449	3	7.7	33	2	S41916	DNA-directed RNA p
450	3	7.7	33	2	S43312	2',3'-cyclic-nucle
451	3	7.7	33	2	A56818	Na+/K+-exchanging
452	3	7.7	33	2	PC2249	peptidylprolyl iso
453	3	7.7	33	2	PC1270	subtilisin inhibit
454	3	7.7	33	2	PC2205	interferon-alpha L
455	3	7.7	33	2	E32502	T-cell receptor de
456	3	7.7	33	2	A31461	T-cell receptor de
457	3	7.7	33	2	A61310	nonhistone chromos
458	3	7.7	33	2	C21211	protamine TP16 - r
459	3	7.7	33	2	E21211	protamine TP21 - r
460	3	7.7	33	2	A26762	protamine (mugilin
461	3	7.7	33	2	B26762	protamine (mugilin
462	3	7.7	33	2	A60601	keratin, 55k, nucl
463	3	7.7	33	2	S50032	lysosomal-associa
464	3	7.7	33	2	A05162	antifreeze protein
465	3	7.7	33	2	I52083	major acute phase
466	3	7.7	33	2	T43305	translation initia
467	3	7.7	33	2	B44906	L1 protein - human
468	3	7.7	33	2	S23321	hypothetical prote
469	3	7.7	33	2	T36211	probable excisiona

470	3	7.7	33	2	I22565	R-phycoerythrin ga
471	3	7.7	33	2	D44798	alkylphosphonate u
472	3	7.7	33	2	S06337	teleocalcin - rain
473	3	7.7	33	2	T08018	ycf12 protein - Ch
474	3	7.7	33	2	I68894	gene TAP1 protein
475	3	7.7	33	2	A87213	hypothetical prote
476	3	7.7	33	2	E84341	hypothetical prote
477	3	7.7	33	2	E43675	orf protein - infe
478	3	7.7	33	2	A70159	hypothetical prote
479	3	7.7	33	2	G70247	hypothetical prote
480	3	7.7	33	2	S61846	hrpY protein - Pse
481	3	7.7	33	2	C82312	hypothetical prote
482	3	7.7	33	2	D82309	hypothetical prote
483	3	7.7	33	2	C82287	hypothetical prote
484	3	7.7	33	2	G82254	hypothetical prote
485	3	7.7	33	2	H82216	hypothetical prote
486	3	7.7	33	2	B82184	hypothetical prote
487	3	7.7	33	2	H82475	hypothetical prote
488	3	7.7	33	2	E82391	hypothetical prote
489	3	7.7	33	2	C82390	hypothetical prote
490	3	7.7	33	2	S63523	formylmethanofuran
491	3	7.7	33	2	T46624	hypothetical prote
492	3	7.7	33	2	A41822	antimicrobial pept
493	3	7.7	33	2	S58578	hypothetical prote
494	3	7.7	33	2	T39160	hypothetical prote
495	3	7.7	33	2	I51869	neurofibromin - hu
496	3	7.7	33	2	S32764	T-cell receptor ga
497	3	7.7	33	2	H43284	zinc finger protei
498	3	7.7	33	2	S68096	lactate dehydrogen
499	3	7.7	33	2	I53301	gene GHR protein -
500	3	7.7	33	2	T03346	gene e21 protein -
501	3	7.7	33	2	E82852	hypothetical prote
502	3	7.7	33	2	E82553	hypothetical prote
503	3	7.7	33	2	C86007	hypothetical prote
504	3	7.7	33	2	F85581	unknown protein en
505	3	7.7	33	2	G86126	hypothetical prote
506	3	7.7	33	2	D89945	hypothetical prote
507	3	7.7	33	2	B81295	probable periplasm
508	3	7.7	33	2	I37258	NADH2 dehydrogenas
509	3	7.7	33	2	C97406	hypothetical prote
510	3	7.7	34	1	LNBOC1	pulmonary surfacta
511	3	7.7	34	2	S27176	cytochrome P450 2E
512	3	7.7	34	2	A12055	glyceraldehyde-3-p
513	3	7.7	34	2	A60475	glyceraldehyde-3-p
514	3	7.7	34	2	S18161	NADH2 dehydrogenas
515	3	7.7	34	2	A60686	cytochrome-c oxida
516	3	7.7	34	2	S62710	cytochrome-c oxida
517	3	7.7	34	2	A28506	pyruvate kinase (E
518	3	7.7	34	2	S08196	3-dehydroquinatate d
519	3	7.7	34	2	I40771	enolase - Campylob
520	3	7.7	34	2	PC1272	subtilisin inhibit
521	3	7.7	34	2	PC1261	alkaline proteinas
522	3	7.7	34	2	PC1267	subtilisin inhibit
523	3	7.7	34	2	A61491	seed protein ws-1
524	3	7.7	34	2	A32271	somatostatin-relat
525	3	7.7	34	2	A40298	dermaseptin - Sauv
526	3	7.7	34	2	C49195	corticostatic pept

527	3	7.7	34	2	A19197	class II histocomp
528	3	7.7	34	2	D60505	hemoglobin A1-4 be
529	3	7.7	34	2	JN0582	protamine (scombr
530	3	7.7	34	2	S20439	protamine - yellow
531	3	7.7	34	2	S56118	myosin II heavy ch
532	3	7.7	34	2	A05330	colipase - chicken
533	3	7.7	34	2	S65716	prostaglandin-D sy
534	3	7.7	34	2	E49410	t-complex polypept
535	3	7.7	34	2	S13439	lectin II, anti-H(
536	3	7.7	34	2	A44806	variant surface gl
537	3	7.7	34	2	S11866	transposase - pear
538	3	7.7	34	2	PS0065	lysis protein t -
539	3	7.7	34	2	D58493	group I allergen D
540	3	7.7	34	2	B60106	type-specific anti
541	3	7.7	34	2	S78345	hypothetical prote
542	3	7.7	34	2	I50713	homeobox protein -
543	3	7.7	34	2	I51364	homeobox protein -
544	3	7.7	34	2	I38900	homeobox protein -
545	3	7.7	34	2	I49145	homeobox protein -
546	3	7.7	34	2	I65263	homeobox protein H
547	3	7.7	34	2	F95129	hypothetical prote
548	3	7.7	34	2	D95208	hypothetical prote
549	3	7.7	34	2	G90912	hypothetical prote
550	3	7.7	34	2	C90973	hypothetical prote
551	3	7.7	34	2	F84466	hypothetical prote
552	3	7.7	34	2	B70230	hypothetical prote
553	3	7.7	34	2	D70249	hypothetical prote
554	3	7.7	34	2	E70255	hypothetical prote
555	3	7.7	34	2	H64666	hypothetical prote
556	3	7.7	34	2	H81883	hypothetical prote
557	3	7.7	34	2	T08490	hypothetical prote
558	3	7.7	34	2	E82284	hypothetical prote
559	3	7.7	34	2	A82048	hypothetical prote
560	3	7.7	34	2	E82458	hypothetical prote
561	3	7.7	34	2	B82449	hypothetical prote
562	3	7.7	34	2	G82415	hypothetical prote
563	3	7.7	34	2	B64015	hypothetical prote
564	3	7.7	34	2	S77646	hypothetical prote
565	3	7.7	34	2	T11814	hypothetical prote
566	3	7.7	34	2	S70330	endosperm protein,
567	3	7.7	34	2	T14642	AW19 protein - sor
568	3	7.7	34	2	S58636	hypothetical prote
569	3	7.7	34	2	A48972	mannose-specific l
570	3	7.7	34	2	S35375	brlA protein - Eme
571	3	7.7	34	2	T19865	hypothetical prote
572	3	7.7	34	2	C31514	hemopexin - chicke
573	3	7.7	34	2	S35923	T-cell receptor ga
574	3	7.7	34	2	F84079	hypothetical prote
575	3	7.7	34	2	B81537	hypothetical prote
576	3	7.7	34	2	E82819	hypothetical prote
577	3	7.7	34	2	B85678	unknown protein en
578	3	7.7	34	2	G85820	unknown protein en
579	3	7.7	34	2	AB2400	cytochrome b6-f co
580	3	7.7	34	4	JT0745	hypothetical trans
581	3	7.7	35	1	HWGHD	exendin-2 - Gila m
582	3	7.7	35	1	LNPGC1	pulmonary surfacta
583	3	7.7	35	1	LNDGC1	pulmonary surfacta

584	3	7.7	35	2	A56859	fatty acid omega-h
585	3	7.7	35	2	S00115	cytochrome-c oxida
586	3	7.7	35	2	S29729	manganese(II) pero
587	3	7.7	35	2	A54257	deoxynucleoside ki
588	3	7.7	35	2	S51708	thioglucohydrolase (E
589	3	7.7	35	2	JN0369	microbial serine p
590	3	7.7	35	2	S42876	probable succinate
591	3	7.7	35	2	D23454	ovalbumin phosphos
592	3	7.7	35	2	S54329	elastase inhibitor
593	3	7.7	35	2	B44800	cryptdin 12 - mous
594	3	7.7	35	2	I48893	cryptdin-10 - mous
595	3	7.7	35	2	I48894	cryptdin-11 - mous
596	3	7.7	35	2	I48898	cryptdin-16 - mous
597	3	7.7	35	2	E38601	Ig kappa chain V r
598	3	7.7	35	2	A05302	hemoglobin beta ch
599	3	7.7	35	2	S27154	ribosomal protein
600	3	7.7	35	2	S07437	ribosomal protein
601	3	7.7	35	2	I55263	alpha-smooth muscl
602	3	7.7	35	2	I39969	outer membrane pro
603	3	7.7	35	2	S61547	transferrin bindin
604	3	7.7	35	2	S19909	E6-III protein - h
605	3	7.7	35	2	PQ0128	hydrogenase matura
606	3	7.7	35	2	T07870	major latex protei
607	3	7.7	35	2	B33770	hypothetical prote
608	3	7.7	35	2	A58493	group I allergen F
609	3	7.7	35	2	F58493	group I allergen A
610	3	7.7	35	2	E58493	group I allergen P
611	3	7.7	35	2	G58493	group I allergen A
612	3	7.7	35	2	PS0439	potassium channel
613	3	7.7	35	2	S20042	hypothetical prote
614	3	7.7	35	2	E64108	protein V6, trunca
615	3	7.7	35	2	H95010	hypothetical prote
616	3	7.7	35	2	F95028	hypothetical prote
617	3	7.7	35	2	F95049	hypothetical prote
618	3	7.7	35	2	H95156	hypothetical prote
619	3	7.7	35	2	B95157	hypothetical prote
620	3	7.7	35	2	F87622	hypothetical prote
621	3	7.7	35	2	B84674	hypothetical prote
622	3	7.7	35	2	H84214	hypothetical prote
623	3	7.7	35	2	C84398	hypothetical prote
624	3	7.7	35	2	S33666	hypothetical prote
625	3	7.7	35	2	B41161	29K antigen PEB2 -
626	3	7.7	35	2	S27307	surface-array prot
627	3	7.7	35	2	C82149	conserved hypothet
628	3	7.7	35	2	D82137	hypothetical prote
629	3	7.7	35	2	F82051	hypothetical prote
630	3	7.7	35	2	B82494	hypothetical prote
631	3	7.7	35	2	B82432	hypothetical prote
632	3	7.7	35	2	S38791	hypothetical prote
633	3	7.7	35	2	JQ2236	hypothetical 4.1K
634	3	7.7	35	2	A05057	hypothetical prote
635	3	7.7	35	2	T07509	photosystem II pro
636	3	7.7	35	2	T10249	lectin homolog 1 -
637	3	7.7	35	2	A33708	thionin, cell wall
638	3	7.7	35	2	JQ0254	hypothetical 4K pr
639	3	7.7	35	2	T06314	alpha-amylase homo
640	3	7.7	35	2	T15713	hypothetical prote

641	3	7.7	35	2	I47076	elastin - sheep (f
642	3	7.7	35	2	A61375	basic fibroblast g
643	3	7.7	35	2	E83824	hypothetical prote
644	3	7.7	35	2	D83924	hypothetical prote
645	3	7.7	35	2	H84034	hypothetical prote
646	3	7.7	35	2	B81570	hypothetical prote
647	3	7.7	35	2	S11614	ribosomal protein
648	3	7.7	35	2	B85708	unknown protein en
649	3	7.7	35	2	F85847	unknown protein en
650	3	7.7	35	2	AI0076	hypothetical prote
651	3	7.7	35	2	A97417	hypothetical prote
652	3	7.7	35	2	AE3041	conserved hypothet
653	3	7.7	35	2	AD2525	hypothetical prote
654	3	7.7	35	4	S41911	hypothetical prote
655	3	7.7	36	1	PCPG	pancreatic hormone
656	3	7.7	36	1	NYPGY	neuropeptide Y - p
657	3	7.7	36	1	PCGXA	pancreatic peptide
658	3	7.7	36	1	PCDFY	pancreatic peptide
659	3	7.7	36	1	PCGS	pancreatic hormone
660	3	7.7	36	1	CKAODP	cecropin D - Chine
661	3	7.7	36	2	F22102	phycoerythrin-545
662	3	7.7	36	2	S21276	glutathione transf
663	3	7.7	36	2	PT0430	leucyl aminopeptid
664	3	7.7	36	2	JQ0365	pancreatic hormone
665	3	7.7	36	2	S07052	neuropeptide Y - s
666	3	7.7	36	2	A30485	neuropeptide Y - r
667	3	7.7	36	2	A28578	pancreatic hormone
668	3	7.7	36	2	B30485	neuropeptide Y - g
669	3	7.7	36	2	A48540	neuropeptide Y - c
670	3	7.7	36	2	A39393	neuropeptide Y - l
671	3	7.7	36	2	A49743	pancreatic peptide
672	3	7.7	36	2	A26377	pancreatic peptide
673	3	7.7	36	2	S27054	neuropeptide Y - A
674	3	7.7	36	2	A59064	egg-laying hormone
675	3	7.7	36	2	F42753	interferon alpha (
676	3	7.7	36	2	JH0721	Ig heavy chain V r
677	3	7.7	36	2	JH0722	Ig H chain V regio
678	3	7.7	36	2	JH0723	Ig heavy chain V r
679	3	7.7	36	2	JH0737	Ig heavy chain V r
680	3	7.7	36	2	PH1753	Ig heavy chain V r
681	3	7.7	36	2	C45875	M1 class I histoco
682	3	7.7	36	2	A29164	cartilage proteogl
683	3	7.7	36	2	S07622	avenin gamma-4 - s
684	3	7.7	36	2	A45798	phosphocarrier pro
685	3	7.7	36	2	B41481	virulence-associat
686	3	7.7	36	2	S00317	photosystem I 11K
687	3	7.7	36	2	S00314	photosystem I chai
688	3	7.7	36	2	A60146	65K heat shock pro
689	3	7.7	36	2	A28503	neuropeptide H - b
690	3	7.7	36	2	S73127	hypothetical prote
691	3	7.7	36	2	S78239	ycf32 protein - Od
692	3	7.7	36	2	T06901	hypothetical prote
693	3	7.7	36	2	H48110	RNA recognition mo
694	3	7.7	36	2	B95156	hypothetical prote
695	3	7.7	36	2	F84791	hypothetical prote
696	3	7.7	36	2	D84275	hypothetical prote
697	3	7.7	36	2	S17834	acetyl-CoA carboxy

698	3	7.7	36	2	E70220	hypothetical prote
699	3	7.7	36	2	H70251	hypothetical prote
700	3	7.7	36	2	A64540	hypothetical prote
701	3	7.7	36	2	F64604	hypothetical prote
702	3	7.7	36	2	T44548	hypothetical prote
703	3	7.7	36	2	A81164	hypothetical prote
704	3	7.7	36	2	S16552	hypothetical prote
705	3	7.7	36	2	G82263	hypothetical prote
706	3	7.7	36	2	B82111	hypothetical prote
707	3	7.7	36	2	D82108	hypothetical prote
708	3	7.7	36	2	G82085	hypothetical prote
709	3	7.7	36	2	D82482	hypothetical prote
710	3	7.7	36	2	D82469	hypothetical prote
711	3	7.7	36	2	D82466	hypothetical prote
712	3	7.7	36	2	D82457	hypothetical prote
713	3	7.7	36	2	A82437	hypothetical prote
714	3	7.7	36	2	E69729	required for trans
715	3	7.7	36	2	S70092	hypothetical prote
716	3	7.7	36	2	S42591	dnaA protein - Str
717	3	7.7	36	2	A69287	hypothetical prote
718	3	7.7	36	2	JA0173	basic peptide - wi
719	3	7.7	36	2	T50336	ribosomal protein
720	3	7.7	36	2	S67795	probable membrane
721	3	7.7	36	2	S78721	protein YGL006w-a
722	3	7.7	36	2	B49139	allergen TBA-1 - T
723	3	7.7	36	2	A61235	fibroblast-activat
724	3	7.7	36	2	B53480	T-cell receptor al
725	3	7.7	36	2	A81740	hypothetical prote
726	3	7.7	36	2	G81734	hypothetical prote
727	3	7.7	36	2	H71293	hypothetical prote
728	3	7.7	36	2	E82854	hypothetical prote
729	3	7.7	36	2	H82703	hypothetical prote
730	3	7.7	36	2	C82694	hypothetical prote
731	3	7.7	36	2	D82617	hypothetical prote
732	3	7.7	36	2	A82598	hypothetical prote
733	3	7.7	36	2	C85910	unknown protein en
734	3	7.7	36	2	AH0066	hypothetical prote
735	3	7.7	36	2	A81309	small hydrophobic
736	3	7.7	36	2	AI1841	hypothetical prote
737	3	7.7	37	1	R5PM81	ribosomal protein
738	3	7.7	37	1	R5EG36	ribosomal protein
739	3	7.7	37	1	R5IT36	ribosomal protein
740	3	7.7	37	1	FDL3W	antifreeze protein
741	3	7.7	37	1	ZJBPF4	gene J protein - p
742	3	7.7	37	1	WRBP65	early protein gp5
743	3	7.7	37	1	WRBPF7	early protein gp5
744	3	7.7	37	2	S73239	plastoquinol-plast
745	3	7.7	37	2	S74215	NADH2 dehydrogenas
746	3	7.7	37	2	S03941	hydrogen dehydroge
747	3	7.7	37	2	S48656	fusicoccin recepto
748	3	7.7	37	2	S03570	trypsin (EC 3.4.21
749	3	7.7	37	2	S02176	acrosin (EC 3.4.21
750	3	7.7	37	2	B38230	inorganic diphosph
751	3	7.7	37	2	A32000	somatostatin, panc
752	3	7.7	37	2	C60580	growth hormone-rel
753	3	7.7	37	2	S26954	peptide YY-related
754	3	7.7	37	2	C32021	bactericidin B-4 -

755	3	7.7	37	2	A32021	bactericidin B-2 -
756	3	7.7	37	2	B32021	bactericidin B-3 -
757	3	7.7	37	2	JH0357	T-cell receptor be
758	3	7.7	37	2	JH0727	Ig heavy chain V r
759	3	7.7	37	2	JH0728	Ig heavy chain V r
760	3	7.7	37	2	JH0729	Ig heavy chain V r
761	3	7.7	37	2	JH0730	Ig heavy chain V r
762	3	7.7	37	2	JH0731	Ig heavy chain V r
763	3	7.7	37	2	JH0734	Ig heavy chain V r
764	3	7.7	37	2	JH0735	Ig heavy chain V r
765	3	7.7	37	2	JH0736	Ig heavy chain V r
766	3	7.7	37	2	JH0738	Ig heavy chain V r
767	3	7.7	37	2	JH0743	Ig heavy chain V r
768	3	7.7	37	2	JH0746	Ig heavy chain V r
769	3	7.7	37	2	JH0747	Ig heavy chain V r
770	3	7.7	37	2	A30607	Ig kappa chain V-I
771	3	7.7	37	2	PS0130	H-2 class I histoc
772	3	7.7	37	2	PS0127	H-2 class I histoc
773	3	7.7	37	2	I48405	histone H2a - mous
774	3	7.7	37	2	S73217	ribosomal protein
775	3	7.7	37	2	B70566	probable ribosomal
776	3	7.7	37	2	E75312	ribosomal protein
777	3	7.7	37	2	T35555	ribosomal protein
778	3	7.7	37	2	D87154	50S ribosomal prot
779	3	7.7	37	2	A57497	agrin-related prot
780	3	7.7	37	2	I51251	myosin heavy chain
781	3	7.7	37	2	I46594	myosin - pig (frag
782	3	7.7	37	2	PC1121	antifungal 25K pro
783	3	7.7	37	2	S17684	thaumatin homolog
784	3	7.7	37	2	A57222	phosphocarrier pro
785	3	7.7	37	2	PS0187	photosystem II oxy
786	3	7.7	37	2	JN0035	early protein gp5
787	3	7.7	37	2	D47099	hypothetical prote
788	3	7.7	37	2	T07292	hypothetical prote
789	3	7.7	37	2	G45187	homeotic protein G
790	3	7.7	37	2	F45187	homeotic protein G
791	3	7.7	37	2	F90765	hypothetical prote
792	3	7.7	37	2	E87618	hypothetical prote
793	3	7.7	37	2	G84233	hypothetical prote
794	3	7.7	37	2	D84284	hypothetical prote
795	3	7.7	37	2	S07517	gene 6.3 protein -
796	3	7.7	37	2	E70241	hypothetical prote
797	3	7.7	37	2	C36727	cytochrome c552 -
798	3	7.7	37	2	S54441	hypothetical prote
799	3	7.7	37	2	C82364	hypothetical prote
800	3	7.7	37	2	H82319	hypothetical prote
801	3	7.7	37	2	A82439	hypothetical prote
802	3	7.7	37	2	B36511	hypothetical prote
803	3	7.7	37	2	S21132	photosystem II cyt
804	3	7.7	37	2	I40568	rap60 regulator ra
805	3	7.7	37	2	S50905	fatty acid beta-ox
806	3	7.7	37	2	T48964	hypothetical prote
807	3	7.7	37	2	T06571	hypothetical prote
808	3	7.7	37	2	S03432	hypothetical prote
809	3	7.7	37	2	A45609	calcium-binding pr
810	3	7.7	37	2	C41933	mating pheromone E
811	3	7.7	37	2	T29808	hypothetical prote

812	3	7.7	37	2	T20564	hypothetical prote
813	3	7.7	37	2	B60529	hemocyanin 4 - edi
814	3	7.7	37	2	S14101	apolipoprotein III
815	3	7.7	37	2	A61438	receptor binding f
816	3	7.7	37	2	C32112	R15 gamma peptide
817	3	7.7	37	2	S03837	hcr protein - wood
818	3	7.7	37	2	I49615	gamma-D-crystallin
819	3	7.7	37	2	B39030	androgen-binding p
820	3	7.7	37	2	E83665	hypothetical prote
821	3	7.7	37	2	C83780	hypothetical prote
822	3	7.7	37	2	A81552	hypothetical prote
823	3	7.7	37	2	E81738	hypothetical prote
824	3	7.7	37	2	B85574	hypothetical prote
825	3	7.7	37	2	H85612	hypothetical prote
826	3	7.7	37	2	G95919	probable transposa
827	3	7.7	37	2	AH0455	hypothetical prote
828	3	7.7	37	2	S70931	histone-like prote
829	3	7.7	37	2	AB0592	probable membrane
830	3	7.7	37	2	AH0637	conserved hypothet
831	3	7.7	37	2	AH0844	hypothetical prote
832	3	7.7	37	2	E97596	hypothetical prote
833	3	7.7	37	4	JE0019	probable 4K protei
834	3	7.7	38	1	HWGHS	exendin-1 - Mexica
835	3	7.7	38	2	S04627	glutathione transf
836	3	7.7	38	2	C34047	stylar glycoprotei
837	3	7.7	38	2	A05222	anthranilate phosp
838	3	7.7	38	2	S39034	lipid transfer pro
839	3	7.7	38	2	A49165	pituitary adenylat
840	3	7.7	38	2	A61070	pituitary adenylat
841	3	7.7	38	2	JH0724	Ig heavy chain V r
842	3	7.7	38	2	JH0725	Ig heavy chain V r
843	3	7.7	38	2	PS0115	H-2 class I histoc
844	3	7.7	38	2	I58994	MHC H2-L transmem
845	3	7.7	38	2	S12409	ribosomal protein
846	3	7.7	38	2	S07140	ribosomal protein
847	3	7.7	38	2	I46861	macrophage migrati
848	3	7.7	38	2	I65220	dopamine D3 recept
849	3	7.7	38	2	I64844	SP-A1 (gamma, delt
850	3	7.7	38	2	PH0104	integrin beta 1 ch
851	3	7.7	38	2	T12207	chaperonin homolog
852	3	7.7	38	2	S78349	photosystem I prot
853	3	7.7	38	2	A59185	photosystem II pro
854	3	7.7	38	2	G45095	photosystem I ligh
855	3	7.7	38	2	JS0456	gene J protein - p
856	3	7.7	38	2	B53708	indolepyruvate syn
857	3	7.7	38	2	A37902	myotrophin - rat (
858	3	7.7	38	2	H95005	hypothetical prote
859	3	7.7	38	2	B95069	hypothetical prote
860	3	7.7	38	2	H91111	hypothetical prote
861	3	7.7	38	2	S07972	regulatory protein
862	3	7.7	38	2	E72306	hypothetical prote
863	3	7.7	38	2	D55543	Tnp protein - Pseu
864	3	7.7	38	2	G81904	hypothetical prote
865	3	7.7	38	2	C81171	hypothetical prote
866	3	7.7	38	2	A47307	heat-stable entero
867	3	7.7	38	2	D82121	hypothetical prote
868	3	7.7	38	2	D82115	hypothetical prote

869	3	7.7	38	2	F82485	hypothetical prote
870	3	7.7	38	2	C82482	hypothetical prote
871	3	7.7	38	2	G64001	hypothetical prote
872	3	7.7	38	2	T36775	hypothetical prote
873	3	7.7	38	2	T37138	hypothetical prote
874	3	7.7	38	2	S61280	nikkomycin synthes
875	3	7.7	38	2	S78357	photosystem II pro
876	3	7.7	38	2	JN0418	hypothetical prote
877	3	7.7	38	2	S55678	calcium-dependent
878	3	7.7	38	2	S14141	hypothetical prote
879	3	7.7	38	2	T04074	transcription acti
880	3	7.7	38	2	T01741	hypothetical prote
881	3	7.7	38	2	S39376	lectin - shallot
882	3	7.7	38	2	S78728	protein YLR264c-a
883	3	7.7	38	2	T15508	hypothetical prote
884	3	7.7	38	2	T34310	hypothetical prote
885	3	7.7	38	2	A32112	R15 alpha 1 osmore
886	3	7.7	38	2	S78757	ribosomal protein
887	3	7.7	38	2	C83729	hypothetical prote
888	3	7.7	38	2	H81603	hypothetical prote
889	3	7.7	38	2	E82858	hypothetical prote
890	3	7.7	38	2	T46593	phytoene dehydroge
891	3	7.7	38	2	A97169	hypothetical prote
892	3	7.7	38	2	E89922	hypothetical prote
893	3	7.7	38	2	T08652	hypothetical prote
894	3	7.7	38	2	AB0747	hypothetical prote
895	3	7.7	38	2	AD0740	hypothetical prote
896	3	7.7	38	2	C97551	hypothetical prote
897	3	7.7	39	1	S28546	protamine 1 - Japa
898	3	7.7	39	1	C69677	phosphatase (RapF)
899	3	7.7	39	2	S65949	hypothetical prote
900	3	7.7	39	2	S33872	glyceraldehyde-3-p
901	3	7.7	39	2	I46149	aldolase A - dog (
902	3	7.7	39	2	I57685	aldolase A - south
903	3	7.7	39	2	S00490	RNA-binding protei
904	3	7.7	39	2	S54330	trypsin inhibitor
905	3	7.7	39	2	I49418	insulin I precurs
906	3	7.7	39	2	D42753	interferon alpha (
907	3	7.7	39	2	E30517	Ig heavy chain pre
908	3	7.7	39	2	PH0878	Ig kappa chain V r
909	3	7.7	39	2	A32934	H-2 class I-like h
910	3	7.7	39	2	S01813	hemoglobin BI - tu
911	3	7.7	39	2	S68791	ribosomal protein
912	3	7.7	39	2	A45479	GTP-binding regula
913	3	7.7	39	2	A38673	G protein alpha i-
914	3	7.7	39	2	A05331	colipase - spiny d
915	3	7.7	39	2	S23804	homeotic protein l
916	3	7.7	39	2	A03353	glutenin 2 - wheat
917	3	7.7	39	2	A54531	circumsporozoite a
918	3	7.7	39	2	E42799	photosystem I chai
919	3	7.7	39	2	S10315	photosystem II pro
920	3	7.7	39	2	S75180	photosystem II pro
921	3	7.7	39	2	AH2286	photosystem II pro
922	3	7.7	39	2	A33975	gag polyprotein -
923	3	7.7	39	2	S77904	tax protein - simi
924	3	7.7	39	2	PS0063	lysis protein t -
925	3	7.7	39	2	G64944	yebJ protein - Esc

926	3	7.7	39	2	A85795	hypothetical prote
927	3	7.7	39	2	S19540	isocitrate dehydro
928	3	7.7	39	2	S78008	fucosyltransferase
929	3	7.7	39	2	S18569	hypothetical prote
930	3	7.7	39	2	S22880	gonadal protein gd
931	3	7.7	39	2	I65265	homeotic protein H
932	3	7.7	39	2	I38143	homeobox - human (
933	3	7.7	39	2	S35325	protein kinase sgg
934	3	7.7	39	2	H95135	hypothetical prote
935	3	7.7	39	2	G90716	probable RNA [impo
936	3	7.7	39	2	C87422	hypothetical prote
937	3	7.7	39	2	C84197	anthranilate synth
938	3	7.7	39	2	G70228	hypothetical prote
939	3	7.7	39	2	B64559	hypothetical prote
940	3	7.7	39	2	G83252	hypothetical prote
941	3	7.7	39	2	E81920	hypothetical prote
942	3	7.7	39	2	A81151	hypothetical prote
943	3	7.7	39	2	A82359	hypothetical prote
944	3	7.7	39	2	H82310	hypothetical prote
945	3	7.7	39	2	G82287	hypothetical prote
946	3	7.7	39	2	F82226	hypothetical prote
947	3	7.7	39	2	B82419	hypothetical prote
948	3	7.7	39	2	S75759	hypothetical prote
949	3	7.7	39	2	S74393	photosystem II Psb
950	3	7.7	39	2	T06940	photosystem II pro
951	3	7.7	39	2	S73118	photosystem II pro
952	3	7.7	39	2	T15158	hypothetical prote
953	3	7.7	39	2	S23803	homeotic protein l
954	3	7.7	39	2	S48644	oxidase - Malayan
955	3	7.7	39	2	I37555	homeobox - human (
956	3	7.7	39	2	I37556	homeobox - human (
957	3	7.7	39	2	S28908	dynein-associated
958	3	7.7	39	2	I46466	luteinizing hormon
959	3	7.7	39	2	D40984	finger protein zfa
960	3	7.7	39	2	B40984	finger protein zfe
961	3	7.7	39	2	I65323	calpain II - rat (
962	3	7.7	39	2	G83716	hypothetical prote
963	3	7.7	39	2	D83721	hypothetical prote
964	3	7.7	39	2	C83904	hypothetical prote
965	3	7.7	39	2	E81540	hypothetical prote
966	3	7.7	39	2	B71285	hypothetical prote
967	3	7.7	39	2	G82733	hypothetical prote
968	3	7.7	39	2	G82718	hypothetical prote
969	3	7.7	39	2	A82707	hypothetical prote
970	3	7.7	39	2	G82619	hypothetical prote
971	3	7.7	39	2	B85609	hypothetical prote
972	3	7.7	39	2	B85990	hypothetical prote
973	3	7.7	39	2	D85649	hypothetical prote
974	3	7.7	39	2	F97313	hypothetical prote
975	3	7.7	39	2	A96026	probable transposa
976	3	7.7	39	2	AC0205	hypothetical prote
977	3	7.7	39	2	F64843	hypothetical prote
978	3	7.7	39	2	G64801	hypothetical prote
979	3	7.7	39	2	AE3109	hypothetical prote
980	3	7.7	39	2	C97513	hypothetical prote
981	3	7.7	39	2	AB1924	photosystem II pro
982	3	7.7	39	2	AB2010	hypothetical prote

983	3	7.7	39	2	AB2552	hypothetical prote
984	3	7.7	40	1	SWFGS	sauvagine - Sauvag
985	3	7.7	40	1	S14717	protamine 2 - Japa
986	3	7.7	40	1	FDFI8G	antifreeze protein
987	3	7.7	40	1	W4BP17	gene 4.1 protein -
988	3	7.7	40	1	A69677	phosphatase (RapC)
989	3	7.7	40	2	S09338	ferredoxin [2Fe-2S
990	3	7.7	40	2	E61320	plastocyanin - Era
991	3	7.7	40	2	E22565	R-phycoerythrin be
992	3	7.7	40	2	B27398	allophycocyanin al
993	3	7.7	40	2	T05931	probable 5-methylt
994	3	7.7	40	2	PQ0533	3-oxoacyl-[acyl-ca
995	3	7.7	40	2	JH0756	sucrose-specific e
996	3	7.7	40	2	A29502	carboxylesterase (
997	3	7.7	40	2	S50021	trypsin-like prote
998	3	7.7	40	2	A49081	capillary permeabi
999	3	7.7	40	2	B41440	protein disulfide-
1000	3	7.7	40	2	S29489	GTP-binding protei

ALIGNMENTS

RESULT 1

G83440

KdpF protein PA1632 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: G83440

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: G83440

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-29 <STO>

A;Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AAG05021.1;

GSPDB:GN00131; PASP:PA1632

A;Experimental source: strain PA01

C;Genetics:

A;Gene: kdpF; PA1632

Query Match 12.8%; Score 5; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5

|||||

Db 8 SLALA 12

RESULT 2

A32860

biotin-binding protein I - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 24-Jun-1993

C;Accession: A32860

R;Bush, L.; White III, H.B.

J. Biol. Chem. 264, 5741-5745, 1989

A;Title: Conversion of domains into subunits in the processing of egg yolk biotin-binding protein I.

A;Reference number: A32860; MUID:89174628; PMID:2925632

A;Accession: A32860

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-29 <BUS>

Query Match 12.8%; Score 5; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADD 7
|||||
Db 23 ALADD 27

RESULT 3

S05124

hypothetical protein 31 - rice chloroplast

C;Species: chloroplast Oryza sativa (rice)

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000

C;Accession: S05124

R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo, C.; Honji, Y.; Sun, C.R.; Meng, B.Y.; Li, Y.Q.; Kanno, A.; Nishizawa, Y.; Hirai, A.; Shinozaki, K.; Sugiura, M.

Mol. Gen. Genet. 217, 185-194, 1989

A;Title: The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.

A;Reference number: S05080; MUID:89364698; PMID:2770692

A;Accession: S05124

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <HIR>

A;Cross-references: EMBL:X15901; NID:g11957; PIDN:CAA33966.1; PID:g12005

A;Note: this sequence was submitted to the EMBL Data Library, July 1989

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 11 LLAAL 15

RESULT 4

S58569

hypothetical protein 31 - maize chloroplast

C;Species: chloroplast Zea mays (maize)

C;Date: 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 29-Oct-1999

C;Accession: S58569

R;Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.

J. Mol. Biol. 251, 614-628, 1995

A;Title: Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing.

A;Reference number: S58531; MUID:95395841; PMID:7666415

A;Accession: S58569

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <MAI>

A;Cross-references: EMBL:X86563; NID:g902200; PIDN:CAA60303.1; PID:g902239

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 11 LLAAL 15

RESULT 5

T14568

hypothetical protein ycf7 - beet chloroplast

C;Species: chloroplast Beta vulgaris (beet)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T14568

R;Ran, Z.; Michaelis, G.

Theor. Appl. Genet. 91, 836-840, 1995

A;Title: Mapping of a chloroplast RFLP marker associated with the CMS cytoplasm of sugar beet (Beta vulgaris).

A;Reference number: Z18144

A;Accession: T14568

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-31 <RAN>

A;Cross-references: EMBL:X87636; NID:g860887; PID:g860889

C;Genetics:

A;Genome: chloroplast

A;Note: ycf7

C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 6

A82451

hypothetical protein VCA0500 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: A82451

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: A82451

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <HEI>

A;Cross-references: GB:AE004381; GB:AE003853; NID:g9657902; PIDN:AAF96403.1; GSPDB:GN00127; TIGR:VCA0500

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0500

A;Map position: 2

Query Match 12.8%; Score 5; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAAF 10
 |||||
 Db 16 DDAAF 20

RESULT 7

G97576

hypothetical protein AGR_C_3308 [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)

C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C;Accession: G97576

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S. Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent
Agrobacterium tumefaciens C58.
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87568.1; PID:g15156908; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_3308
A;Map position: circular chromosome

Query Match 12.8%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
||||
Db 16 KLLVL 20

RESULT 8

T14210

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain_1 - Uromastyx acanthinurus
mitochondrion (fragment)

C;Species: mitochondrion Uromastyx acanthinurus

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002

C;Accession: T14210

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A;Title: Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome.

A;Reference number: Z17789; MUID:97153826; PMID:9000757

A;Accession: T14210

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <MAC>

A;Cross-references: EMBL:U71325; NID:g1753264; PID:g1753265; PIDN:AAC62247.1

A;Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology,
University of California at Berkeley

C;Genetics:

A;Genome: mitochondrion

A;Note: ND1

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative
phosphorylation; oxidoreductase; respiratory chain

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
||||
Db 20 LAAL 23

RESULT 9

S21278

glutathione transferase (EC 2.5.1.18) alpha-Yx - rat (fragment)

N;Alternate names: glutathione S-transferase Yx; glutathione transferase Yfetus

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998

C;Accession: S21278

R;Igarashi, T.; Tsuchiya, T.; Shikata, Y.; Sagami, F.; Tagaya, O.; Horie, T.; Satoh, T.

Biochem. J. 283, 307-311, 1992

A;Title: Developmental aspects of a unique glutathione S-transferase subunit Yx in the liver cytosol from rats with hereditary hyperbilirubinuria. Comparison with rat fetal liver transferase subunit Yfetus.

A;Reference number: S21278; MUID:92231842; PMID:1567376

A;Accession: S21278

A;Molecule type: protein

A;Residues: 1-28 <IGA>

C;Superfamily: glutathione transferase

C;Keywords: dimer; liver; transferase

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAA 19
|||
Db 21 LLAA 24

RESULT 10

B35948

phospholipase A2 (EC 3.1.1.4) 2 - black-banded coral snake (fragment)

C;Species: Micrurus nigrocinctus (black-banded coral snake)

C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 12-Apr-1995

C;Accession: B35948

R;Mochca-Morales, J.; Martin, B.M.; Zamudio, F.Z.; Possani, L.D.

Toxicon 28, 616-617, 1990

A;Title: Isolation and characterization of three toxic phospholipases from the venom of the coral snake Micrurus nigrocinctus.

A;Reference number: A35948

A;Accession: B35948

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <MOC>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 RHWL 26
|||
Db 15 RHWL 18

RESULT 11

A56366

intestinal trefoil factor - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999

C;Accession: A56366

R;Sands, B.E.; Ogata, H.; Lynch-Devaney, K.; deBeaumont, M.; Ezzell, R.M.; Podolsky, D.K.

J. Biol. Chem. 270, 9353-9361, 1995

A;Title: Molecular cloning of the rat intestinal trefoil factor gene.

Characterization of an intestinal goblet cell-associated promoter.

A;Reference number: A56366; MUID:95238450; PMID:7721858

A;Accession: A56366

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <RES>

A;Cross-references: EMBL:U20984; NID:g930338; PIDN:AAB01063.1; PID:g930339

C;Superfamily: secretory protein xP1; trefoil homology

C;Keywords: intestine

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 11 LLVL 14

RESULT 12

PH0231

T-cell receptor Vb CDR3, carrier PBL Vb 6.sbt - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 30-May-1997

C;Accession: PH0231

R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.;

Akizuki, S.; Goto, I.; Watanabe, T.

submitted to JIPID, June 1994

A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor Vb CDR3 sequences in spinal cord lesions of HTLV-I associated myelopathy/Tropical spastic paraparesis.

A;Reference number: PH0227

A;Accession: PH0231

A;Molecule type: mRNA

A;Residues: 1-28 <HAR>

A;Experimental source: spinal cord

C;Genetics:

A;Map position: 7

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: receptor

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 20 LLVL 23

RESULT 13

T06925

hypothetical protein L - Cyanophora paradoxa cyanelle

C;Species: cyanelle Cyanophora paradoxa

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999

C;Accession: T06925

R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A;Reference number: Z15840

A;Accession: T06925

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <STI>

A;Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81268.1; PID:g1016181

A;Experimental source: strain Pringsheim LB55

C;Genetics:

A;Gene: petL

A;Genome: cyanelle

C;Keywords: cyanelle

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 14 LALA 17

RESULT 14

JQ1035

hypothetical 3.2K protein (type I IGFR 5' region) - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: JQ1035

R;Cooke, D.W.; Bankert, L.A.; Roberts Jr., C.T.; LeRoith, D.; Casella, S.J. Biochem. Biophys. Res. Commun. 177, 1113-1120, 1991

A;Title: Analysis of the human type I insulin-like growth factor receptor promotor region.

A;Reference number: PQ0159; MUID:91282751; PMID:1711844

A;Accession: JQ1035

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <COO>

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDA 8
|||
Db 3 ADDA 6

RESULT 15

E47719

house-dust-mite-reactive T-cell receptor beta chain (CD4+ clone DE26, V(D)J junctional region) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: E47719

R;Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.

Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993

A;Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell recognition of house dust mite allergens.

A;Reference number: A47719; MUID:93376774; PMID:8367485

A;Accession: E47719

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-29 <WED>

A;Note: sequence extracted from NCBI backbone (NCBIN:137825, NCBIP:137831)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 22 LLVL 25

RESULT 16

S58390

T-cell receptor beta-chain Vb6-Jb2.5 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999

C;Accession: S58390

R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.

Nucleic Acids Res. 23, 3074-3075, 1995

A;Title: A novel method for sequencing members of multi-gene families.

A;Reference number: S58384; MUID:95388532; PMID:7659534

A;Accession: S58390

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-29 <JOH>

A;Cross-references: EMBL:U20304; NID:g663131; PIDN:AAA62251.1; PID:g663132

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

A;Note: only a part of the coding sequence is given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||

Db 26 LLVL 29

RESULT 17

I37534

gene HLA-DRB protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999

C;Accession: I37534

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37534

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65585; NID:g296296; PIDN:CAA46544.1; PID:g296297

C;Genetics:

A;Gene: HLA-DRB

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 26 LALA 29

RESULT 18

I37535

gene HLA-DRB protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999

C;Accession: I37535

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37535

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65586; NID:g296298; PIDN:CAA46545.1; PID:g296299

C;Genetics:

A;Gene: HLA-DRB

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5

Db |||||
 26 LALA 29

RESULT 19

I37536
MHC class II histocompatibility antigen HLA-DRB1*0401 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: I37536
R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993
A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.
A;Reference number: I37300; MUID:93216303; PMID:8462990
A;Accession: I37536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: EMBL:X65587; NID:g296300; PIDN:CAA46546.1; PID:g296301
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
 |||||
Db 26 LALA 29

RESULT 20

I37301
MHC class II histocompatibility antigen HLA-DR beta-3 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: I37301; I37302
R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993
A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.
A;Reference number: I37300; MUID:93216303; PMID:8462990
A;Accession: I37301
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: EMBL:X65558; NID:g296268; PIDN:CAA46528.1; PID:g296269
A;Note: this allele is designated DRB3*0101
A;Accession: I37302
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <RE2>
A;Cross-references: EMBL:X65559; NID:g296270; PIDN:CAA46529.1; PID:g296271
A;Note: this allele is designated DRB3*0201
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 12 LAAL 15

RESULT 21

I37303

HLA-DR beta - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C;Accession: I37303; I37305

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37303

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X64544; NID:g296276; PIDN:CAA45842.1; PID:g296277

A;Accession: I37305

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RE2>

A;Cross-references: EMBL:X64548; NID:g296280; PIDN:CAA45846.1; PID:g296281

C;Genetics:

A;Gene: GDB:HLA-DRB5

A;Cross-references: GDB:125658

A;Map position: 6p21.3-6p21.3

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 26 LALA 29

RESULT 22

I37306

HLA-DR beta - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C;Accession: I37306

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37306

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: EMBL:X64549; NID:g296282; PIDN:CAA45847.1; PID:g296283
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
 ||||
Db 26 LALA 29

RESULT 23

S78326

conserved hypothetical protein 29 - *Odontella sinensis* chloroplast

C;Species: chloroplast *Odontella sinensis*

C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998

C;Accession: S78326

R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.

Plant Mol. Biol. Rep. 13, 336-342, 1995

A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, *Odontella sinensis*.

A;Reference number: S78238

A;Accession: S78326

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-29 <KOW>

A;Cross-references: EMBL:Z67753; NID:g1185127; PID:e211871; PID:g1185216

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C;Genetics:

A;Gene: ycf6

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
 ||||
Db 18 SLAL 21

RESULT 24

S16323

hypothetical protein - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000

C;Accession: S16323

R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A;Title: A novel class of plant proteins containing a homeodomain with a closely linked leucine zipper motif.

A;Reference number: S16323; MUID:91266907; PMID:1675603

A;Accession: S16323
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-29 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41623.1; PID:g16328

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ARLL 17
|||
Db 13 ARLL 16

RESULT 25

S78714
protein YDR524w-a - yeast (*Saccharomyces cerevisiae*)
C;Species: *Saccharomyces cerevisiae*
C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999
C;Accession: S78714
R;Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A;Description: The sequence of *S. cerevisiae* cosmids 8166, 9787, 9717, and
lambda 3073.
A;Reference number: S69553
A;Accession: S78714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-29 <DIE>
A;Cross-references: EMBL:U33057; MIPS:YDR524w-a
C;Genetics:
A;Map position: 4R

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLVL 36
|||
Db 26 LLVL 29

RESULT 26

S21195
spectrin beta chain - pig
C;Species: *Sus scrofa domestica* (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S21195
R;Frappier, T.; Derancourt, J.; Pradel, L.A.
Eur. J. Biochem. 205, 85-91, 1992
A;Title: Actin and neurofilament binding domain of brain spectrin beta subunit.
A;Reference number: S21195; MUID:92209538; PMID:1555607
A;Accession: S21195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 <FRA>

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology;
spectrin/dystrophin repeat homology; WW repeat homology

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALAD 6
|||
Db 1 ALAD 4

RESULT 27

S30333

N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.--) - Comamonas sp. (fragment)

C;Species: Comamonas sp.

C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000

C;Accession: S30333

R;Ogawa, J.; Shimizu, S.; Yamada, H.

Eur. J. Biochem. 212, 685-691, 1993

A;Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c.
Purification and characterization.

A;Reference number: S30333; MUID:93215645; PMID:8462543

A;Accession: S30333

A;Molecule type: protein

A;Residues: 1-30 <OGA>

A;Experimental source: strain E222c

C;Function:

A;Description: amidohydrolase with strict specificity for the D-form and strict
substrate specificity for N-carbamoyl-D-amino acids, no reaction with substrates
like N-carbamoyl-beta-alanine or N-carbamoyl-DL-aspartate

C;Superfamily: hypothetical protein YLR351c

C;Keywords: hydrolase

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLLA 18
|||
Db 26 RLLA 29

RESULT 28

E84786

hypothetical protein At2g36940 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: E84786

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <STO>
A;Cross-references: GB:AE002093; NID:g4883610; PIDN:AAD31579.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36940
A;Map position: 2

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
 ||||
Db 9 SLAL 12

RESULT 29

PH0236

T-cell receptor Vb CDR3, Ctr2 TCR Vb12 CDR 3aa.sbt - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-May-1997

C;Accession: PH0236

R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.;

Akizuki, S.; Goto, I.; Watanabe, T.

submitted to JIPID, June 1994

A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor Vb CDR3 sequences in spinal cord lesions of HTLV-I associated myelopathy/Tropical spastic paraparesis.

A;Reference number: PH0227

A;Accession: PH0236

A;Molecule type: mRNA

A;Residues: 1-31 <HAR>

A;Experimental source: spinal cord

C;Genetics:

A;Map position: 7

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: receptor

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
 ||||
Db 23 LLVL 26

RESULT 30

I48082

mitochondrial benzodiazepine receptor - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C;Accession: I48082
R;Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.
Gene 155, 201-205, 1995
A;Title: Comparison of repetitive elements in the third intron of human and rodent mitochondrial benzodiazepine receptor-encoding genes.
A;Reference number: I38724; MUID:95237610; PMID:7721091
A;Accession: I48082
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: EMBL:U12420; NID:g529943; PIDN:AAA83251.1; PID:g1039378
C;Genetics:
A;Gene: MBR
A;Introns: 13/3
C;Superfamily: peripheral-type benzodiazepine receptor
C;Keywords: mitochondrion

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALAD 6
|||
Db 14 ALAD 17

RESULT 31

S76281

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S76281

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76281

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-31 <KAN>

A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10133.1; PID:d1010784; PID:g1673336

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRE 12
|||

Db

22 AFRE 25

RESULT 32

S74965

photosystem I reaction center chain psaM - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein smr0005

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S74965

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S74965

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KAN>

A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA17005.1;

PID:d1017738; PID:g1652080

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: psaM

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20

||||

Db 9 LAAL 12

RESULT 33

D82827

hypothetical protein XF0271 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: D82827

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: D82827

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-31 <SIM>

A;Cross-references: GB:AE003880; GB:AE003849; NID:g9105080; PIDN:AAF83084.1;
GSPDB:GN00128; XFSC:XF0271

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.;
Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros,
M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.;
Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.;
Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.;
Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.;
Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco,
M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.;
Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper,
E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.;
Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado,
J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques,
M.V.; Martins, E.A.L.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.;
Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento,
A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira,
M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto,
B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.;
Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.;
Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da
Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza,
A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tsuhako, M.H.; Vallada, H.; Van
Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.;
Meidanis, J.; Setubal, J.C.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0271

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Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
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Db 23 SLAL 26

RESULT 34

T07290

photosystem I protein psaM - *Chlorella vulgaris* chloroplast

C;Species: chloroplast *Chlorella vulgaris*

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C;Accession: T07290

R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki,
J.; Nakashima, K.; Tsudzuki, T.; Suzuki, Y.; Hamada, A.; Ohta, T.; Inamura, A.;
Yoshinaga, K.; Sugiura, M.

Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A;Title: Complete nucleotide sequence of the chloroplast genome from the green
alga *Chlorella vulgaris*: the existence of genes possibly involved in chloroplast
division.

A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57938.1; PID:g2224454
C;Genetics:
A;Gene: psaM
A;Genome: chloroplast
C;Keywords: chloroplast; membrane-associated complex; photosynthesis;
photosystem I; thylakoid

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 14 LALA 17

RESULT 35

D61014

defensin NP-1 - rat

N;Alternate names: cationic cysteine-rich peptide R-4

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: D61014; A60113

R;Belcourt, D.; Singh, A.; Bateman, A.; Lazure, C.; Solomon, S.; Bennett, H.P.J.
Regul. Pept. 40, 87-100, 1992

A;Title: Purification of cationic cystine-rich peptides from rat bone marrow.
Primary structures and biological activity of the rat corticostatin family of
peptides.

A;Reference number: A61014; MUID:93067247; PMID:1332140

A;Accession: D61014

A;Molecule type: protein

A;Residues: 1-32 <BEL>

R;Eisenhauer, P.B.; Harwig, S.L.; Szklarek, D.; Ganz, T.; Selsted, M.E.; Lehrer,
R.I.

Infect. Immun. 57, 2021-2027, 1989

A;Title: Purification and antimicrobial properties of three defensins from rat
neutrophils.

A;Reference number: A60113; MUID:89277517; PMID:2543629

A;Accession: A60113

A;Molecule type: protein

A;Residues: 1-32 <EIS>

C;Comment: Defensins are antimicrobial cationic peptides with activity against
fungi and bacteria.

C;Superfamily: mammalian defensin

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRER 13
|||
Db 12 FRER 15

RESULT 36

E61014

defensin R-5 - rat

N;Alternate names: cationic cysteine-rich peptide R-5

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: E61014

R;Belcourt, D.; Singh, A.; Bateman, A.; Lazure, C.; Solomon, S.; Bennett, H.P.J.

Regul. Pept. 40, 87-100, 1992

A;Title: Purification of cationic cystine-rich peptides from rat bone marrow. Primary structures and biological activity of the rat corticostatin family of peptides.

A;Reference number: A61014; MUID:93067247; PMID:1332140

A;Accession: E61014

A;Molecule type: protein

A;Residues: 1-32 <BEL>

C;Comment: Defensins are antimicrobial cationic peptides with activity against fungi and bacteria.

C;Superfamily: mammalian defensin

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRER 13
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Db 12 FRER 15

RESULT 37

A25735

interphotoreceptor retinoid-binding protein - rhesus macaque (fragment)

N;Alternate names: interstitial retinol-binding protein

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 21-Nov-1997

C;Accession: A25735; E24417

R;Redmond, T.M.; Wiggert, B.; Robey, F.A.; Chader, G.J.

Biochem. J. 240, 19-26, 1986

A;Title: Interspecies conservation of structure of interphotoreceptor retinoid-binding protein. Similarities and differences as adjudged by peptide mapping and N-terminal sequencing.

A;Reference number: A90335; MUID:87156570; PMID:3827838

A;Accession: A25735

A;Molecule type: protein

A;Residues: 1-32 <RED>

R;Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.

FEBS Lett. 205, 309-312, 1986

A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.

A;Reference number: A91365; MUID:86301171; PMID:3743780

A;Accession: E24417

A;Molecule type: protein

A;Residues: 1-4,'X',6-22 <FON>

C;Superfamily: interphotoreceptor retinoid-binding protein

C;Keywords: duplication

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LVLD 37
||||
Db 10 LVLD 13

RESULT 38

C84355

hypothetical protein Vng2049c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: C84355

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrojna, J.; Swartzell, S.; Weir, D.;
Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: C84355

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-32 <STO>

A;Cross-references: GB:AE004437; NID:g10581474; PIDN:AAG20207.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG2049C

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERA 14
||||
Db 15 RERA 18

RESULT 39

PC7067

meltrin beta - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 20-Jun-2000

C;Accession: PC7067

R;Kurohara, K.; Matsuda, Y.; Nagabukuro, A.; Tsuji, A.; Amagasa, T.; Fujisawa-
Sehara, A.

Biochem. Biophys. Res. Commun. 270, 522-527, 2000

A;Title: Meltrin beta (ADAM19) gene: Cloning, mapping, and analysis of the
regulatory region.

A;Reference number: PC7067

A;Accession: PC7067
A;Molecule type: mRNA
A;Residues: 1-32 <KUR>
C;Comment: This protein, a member of the membrane-bound metalloprotease-disintegrin family, functions in the morphogenesis.
C;Genetics:
A;Map position: 11A5-B1.1
C;Keywords: membrane bound; metalloproteinase

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 13 LALA 16

RESULT 40

A44181
Cerastes serine proteinase (EC 3.4.21.-) - horn viper (fragment)
N;Alternate names: proteinase RP34
C;Species: Cerastes cerastes (horn viper)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-May-2000
C;Accession: A44181
R;Laraba-Djebari, F.; Martin-Eauclaire, M.F.; Marchot, P.
Toxicon 30, 1399-1410, 1992
A;Title: A fibrinogen-clotting serine proteinase from Cerastes cerastes (horned viper) venom with arginine-esterase and amidase activities. Purification, characterization and kinetic parameter determination.
A;Reference number: A44181; MUID:93134605; PMID:1485336
A;Accession: A44181
A;Molecule type: protein
A;Residues: 1-33 <LAR>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:122484)
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; venom

Query Match 10.3%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
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Db 14 SLAL 17

Search completed: January 14, 2004, 10:37:36
Job time : 15.5421 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 26.243 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL DAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	39	100.0	39	11	US-09-843-221A-160	Sequence 160, App
2	39	100.0	39	11	US-09-843-221A-170	Sequence 170, App
3	39	100.0	39	15	US-10-014-162-1	Sequence 1, Appli
4	38	97.4	38	15	US-10-014-162-2	Sequence 2, Appli
5	38	97.4	38	15	US-10-014-162-38	Sequence 38, Appl
6	37	94.9	37	15	US-10-014-162-3	Sequence 3, Appli
7	37	94.9	37	15	US-10-014-162-39	Sequence 39, Appl
8	36	92.3	36	15	US-10-014-162-4	Sequence 4, Appli
9	36	92.3	36	15	US-10-014-162-40	Sequence 40, Appl
10	35	89.7	35	15	US-10-014-162-5	Sequence 5, Appli
11	35	89.7	35	15	US-10-014-162-41	Sequence 41, Appl
12	34	87.2	34	15	US-10-014-162-6	Sequence 6, Appli
13	34	87.2	34	15	US-10-014-162-42	Sequence 42, Appl
14	33	84.6	33	15	US-10-014-162-7	Sequence 7, Appli
15	33	84.6	33	15	US-10-014-162-43	Sequence 43, Appl
16	32	82.1	32	15	US-10-014-162-8	Sequence 8, Appli
17	32	82.1	32	15	US-10-014-162-44	Sequence 44, Appl
18	31	79.5	31	15	US-10-014-162-9	Sequence 9, Appli
19	31	79.5	31	15	US-10-014-162-45	Sequence 45, Appl
20	31	79.5	31	15	US-10-014-162-78	Sequence 78, Appl
21	30	76.9	30	15	US-10-014-162-10	Sequence 10, Appl
22	30	76.9	30	15	US-10-014-162-46	Sequence 46, Appl
23	30	76.9	30	15	US-10-014-162-79	Sequence 79, Appl
24	29	74.4	29	15	US-10-014-162-11	Sequence 11, Appl
25	29	74.4	29	15	US-10-014-162-47	Sequence 47, Appl
26	29	74.4	29	15	US-10-014-162-80	Sequence 80, Appl
27	28	71.8	28	15	US-10-014-162-48	Sequence 48, Appl
28	6	15.4	28	12	US-10-154-884B-11122	Sequence 11122, A
29	6	15.4	31	12	US-10-154-884B-11106	Sequence 11106, A
30	6	15.4	37	15	US-10-026-741-7	Sequence 7, Appli
31	6	15.4	38	9	US-09-779-451-40	Sequence 40, Appl
32	5	12.8	28	9	US-09-864-761-37845	Sequence 37845, A
33	5	12.8	28	9	US-09-864-761-38197	Sequence 38197, A
34	5	12.8	28	9	US-09-864-761-45958	Sequence 45958, A
35	5	12.8	28	9	US-09-782-980-145	Sequence 145, App
36	5	12.8	28	11	US-09-776-724A-114	Sequence 114, App
37	5	12.8	28	14	US-10-001-887-123	Sequence 123, App
38	5	12.8	29	10	US-09-905-831-12	Sequence 12, Appl
39	5	12.8	29	10	US-09-905-831-14	Sequence 14, Appl
40	5	12.8	29	10	US-09-905-831-15	Sequence 15, Appl
41	5	12.8	29	11	US-09-259-658-15	Sequence 15, Appl
42	5	12.8	29	11	US-09-820-843A-22	Sequence 22, Appl
43	5	12.8	29	11	US-09-491-614-14	Sequence 14, Appl
44	5	12.8	29	11	US-09-491-614-15	Sequence 15, Appl
45	5	12.8	29	15	US-10-103-597A-8	Sequence 8, Appli
46	5	12.8	29	15	US-10-161-205-13	Sequence 13, Appl
47	5	12.8	29	15	US-10-101-001-13	Sequence 13, Appl
48	5	12.8	29	15	US-10-188-444-8	Sequence 8, Appli
49	5	12.8	30	12	US-09-933-767-614	Sequence 614, App
50	5	12.8	30	15	US-10-023-282-614	Sequence 614, App
51	5	12.8	32	9	US-09-791-946-3	Sequence 3, Appli
52	5	12.8	32	12	US-10-164-279-11	Sequence 11, Appl
53	5	12.8	32	12	US-09-791-551-33	Sequence 33, Appl
54	5	12.8	33	9	US-09-864-761-33569	Sequence 33569, A
55	5	12.8	33	12	US-10-164-279-2	Sequence 2, Appli
56	5	12.8	35	12	US-10-153-244-319	Sequence 319, App

57	5	12.8	35	12	US-10-153-244-333	Sequence 333, App
58	5	12.8	35	12	US-10-264-049-3193	Sequence 3193, App
59	5	12.8	37	9	US-09-864-761-34924	Sequence 34924, A
60	5	12.8	38	10	US-09-919-473-12	Sequence 12, Appl
61	5	12.8	38	12	US-10-029-386-31288	Sequence 31288, A
62	5	12.8	38	15	US-10-099-766-6	Sequence 6, Appli
63	5	12.8	39	9	US-09-864-761-44798	Sequence 44798, A
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66	5	12.8	39	12	US-10-315-964A-288	Sequence 288, App
67	5	12.8	39	12	US-10-317-251A-287	Sequence 287, App
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69	5	12.8	39	12	US-10-317-252A-287	Sequence 287, App
70	5	12.8	39	12	US-10-317-252A-288	Sequence 288, App
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73	5	12.8	40	12	US-10-315-964A-21	Sequence 21, Appl
74	5	12.8	40	12	US-10-315-964A-23	Sequence 23, Appl
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76	5	12.8	40	12	US-10-315-964A-281	Sequence 281, App
77	5	12.8	40	12	US-10-315-964A-282	Sequence 282, App
78	5	12.8	40	12	US-10-315-964A-285	Sequence 285, App
79	5	12.8	40	12	US-10-315-964A-286	Sequence 286, App
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81	5	12.8	40	12	US-10-315-964A-290	Sequence 290, App
82	5	12.8	40	12	US-10-315-964A-291	Sequence 291, App
83	5	12.8	40	12	US-10-315-964A-292	Sequence 292, App
84	5	12.8	40	12	US-10-315-964A-294	Sequence 294, App
85	5	12.8	40	12	US-10-315-964A-295	Sequence 295, App
86	5	12.8	40	12	US-10-315-964A-373	Sequence 373, App
87	5	12.8	40	12	US-10-315-964A-375	Sequence 375, App
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89	5	12.8	40	12	US-10-315-964A-378	Sequence 378, App
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96	5	12.8	40	12	US-10-317-251A-281	Sequence 281, App
97	5	12.8	40	12	US-10-317-251A-282	Sequence 282, App
98	5	12.8	40	12	US-10-317-251A-285	Sequence 285, App
99	5	12.8	40	12	US-10-317-251A-286	Sequence 286, App
100	5	12.8	40	12	US-10-317-251A-289	Sequence 289, App
101	5	12.8	40	12	US-10-317-251A-290	Sequence 290, App
102	5	12.8	40	12	US-10-317-251A-291	Sequence 291, App
103	5	12.8	40	12	US-10-317-251A-292	Sequence 292, App
104	5	12.8	40	12	US-10-317-251A-294	Sequence 294, App
105	5	12.8	40	12	US-10-317-251A-295	Sequence 295, App
106	5	12.8	40	12	US-10-317-251A-373	Sequence 373, App
107	5	12.8	40	12	US-10-317-251A-375	Sequence 375, App
108	5	12.8	40	12	US-10-317-251A-377	Sequence 377, App
109	5	12.8	40	12	US-10-317-251A-378	Sequence 378, App
110	5	12.8	40	12	US-10-317-251A-379	Sequence 379, App
111	5	12.8	40	12	US-10-317-251A-381	Sequence 381, App
112	5	12.8	40	12	US-10-317-251A-383	Sequence 383, App
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122	5	12.8	40	12	US-10-317-252A-291	Sequence 291, App
123	5	12.8	40	12	US-10-317-252A-292	Sequence 292, App
124	5	12.8	40	12	US-10-317-252A-294	Sequence 294, App
125	5	12.8	40	12	US-10-317-252A-295	Sequence 295, App
126	5	12.8	40	12	US-10-317-252A-373	Sequence 373, App
127	5	12.8	40	12	US-10-317-252A-375	Sequence 375, App
128	5	12.8	40	12	US-10-317-252A-377	Sequence 377, App
129	5	12.8	40	12	US-10-317-252A-378	Sequence 378, App
130	5	12.8	40	12	US-10-317-252A-379	Sequence 379, App
131	5	12.8	40	12	US-10-317-252A-381	Sequence 381, App
132	5	12.8	40	12	US-10-317-252A-383	Sequence 383, App
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144	4	10.3	28	9	US-09-929-818-138	Sequence 138, App
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150	4	10.3	28	11	US-09-305-736-345	Sequence 345, App
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153	4	10.3	28	12	US-09-882-171-520	Sequence 520, App
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204	4	10.3	29	12	US-10-253-471-1393	Sequence 1393, Ap
205	4	10.3	29	12	US-10-253-471-1432	Sequence 1432, Ap
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215	4	10.3	29	15	US-10-188-444-9	Sequence 9, Appli
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225	4	10.3	30	11	US-09-809-391-443	Sequence 443, App
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233	4	10.3	30	12	US-10-192-832-59	Sequence 59, Appl
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316	4	10.3	32	15	US-10-174-410-263	Sequence 263, App
317	4	10.3	32	15	US-10-052-942-54	Sequence 54, Appl
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948	3	7.7	28	9	US-09-929-818-16	Sequence 16, Appl
949	3	7.7	28	9	US-09-929-818-17	Sequence 17, Appl
950	3	7.7	28	9	US-09-929-818-18	Sequence 18, Appl
951	3	7.7	28	9	US-09-929-818-19	Sequence 19, Appl
952	3	7.7	28	9	US-09-929-818-21	Sequence 21, Appl
953	3	7.7	28	9	US-09-929-818-22	Sequence 22, Appl
954	3	7.7	28	9	US-09-929-818-26	Sequence 26, Appl
955	3	7.7	28	9	US-09-929-818-27	Sequence 27, Appl
956	3	7.7	28	9	US-09-929-818-28	Sequence 28, Appl
957	3	7.7	28	9	US-09-929-818-29	Sequence 29, Appl
958	3	7.7	28	9	US-09-929-818-30	Sequence 30, Appl
959	3	7.7	28	9	US-09-929-818-31	Sequence 31, Appl
960	3	7.7	28	9	US-09-929-818-32	Sequence 32, Appl
961	3	7.7	28	9	US-09-929-818-33	Sequence 33, Appl
962	3	7.7	28	9	US-09-929-818-34	Sequence 34, Appl
963	3	7.7	28	9	US-09-929-818-35	Sequence 35, Appl
964	3	7.7	28	9	US-09-929-818-36	Sequence 36, Appl
965	3	7.7	28	9	US-09-929-818-37	Sequence 37, Appl
966	3	7.7	28	9	US-09-929-818-38	Sequence 38, Appl
967	3	7.7	28	9	US-09-929-818-39	Sequence 39, Appl
968	3	7.7	28	9	US-09-929-818-40	Sequence 40, Appl

969	3	7.7	28	9	US-09-929-818-41	Sequence 41, Appl
970	3	7.7	28	9	US-09-929-818-43	Sequence 43, Appl
971	3	7.7	28	9	US-09-929-818-44	Sequence 44, Appl
972	3	7.7	28	9	US-09-929-818-45	Sequence 45, Appl
973	3	7.7	28	9	US-09-929-818-46	Sequence 46, Appl
974	3	7.7	28	9	US-09-929-818-47	Sequence 47, Appl
975	3	7.7	28	9	US-09-929-818-48	Sequence 48, Appl
976	3	7.7	28	9	US-09-929-818-49	Sequence 49, Appl
977	3	7.7	28	9	US-09-929-818-50	Sequence 50, Appl
978	3	7.7	28	9	US-09-929-818-51	Sequence 51, Appl
979	3	7.7	28	9	US-09-929-818-52	Sequence 52, Appl
980	3	7.7	28	9	US-09-929-818-53	Sequence 53, Appl
981	3	7.7	28	9	US-09-929-818-54	Sequence 54, Appl
982	3	7.7	28	9	US-09-929-818-61	Sequence 61, Appl
983	3	7.7	28	9	US-09-929-818-62	Sequence 62, Appl
984	3	7.7	28	9	US-09-929-818-66	Sequence 66, Appl
985	3	7.7	28	9	US-09-929-818-69	Sequence 69, Appl
986	3	7.7	28	9	US-09-929-818-76	Sequence 76, Appl
987	3	7.7	28	9	US-09-929-818-77	Sequence 77, Appl
988	3	7.7	28	9	US-09-929-818-80	Sequence 80, Appl
989	3	7.7	28	9	US-09-929-818-87	Sequence 87, Appl
990	3	7.7	28	9	US-09-929-818-94	Sequence 94, Appl
991	3	7.7	28	9	US-09-929-818-95	Sequence 95, Appl
992	3	7.7	28	9	US-09-929-818-97	Sequence 97, Appl
993	3	7.7	28	9	US-09-929-818-99	Sequence 99, Appl
994	3	7.7	28	9	US-09-929-818-100	Sequence 100, App
995	3	7.7	28	9	US-09-929-818-101	Sequence 101, App
996	3	7.7	28	9	US-09-929-818-102	Sequence 102, App
997	3	7.7	28	9	US-09-929-818-103	Sequence 103, App
998	3	7.7	28	9	US-09-929-818-104	Sequence 104, App
999	3	7.7	28	9	US-09-929-818-105	Sequence 105, App
1000	3	7.7	28	15	US-10-216-209-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-843-221A-160

; Sequence 160, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 3

US-10-014-162-1

; Sequence 1, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-1

Query Match 100.0%; Score 39; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 4

US-10-014-162-2

; Sequence 2, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Bos taurus

B 15. I

LVLDA P 3

B 15. T

LJVLDA 3


```
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-4
```

```
Query Match          92.3%; Score 36; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
          |||
Db      1 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 36
```

RESULT 9

```
US-10-014-162-40
; Sequence 40, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-40
```

```
Query Match          92.3%; Score 36; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36
          |||
Db      1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36
```

RESULT 10

US-10-014-162-5

; Sequence 5, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 35
 ; TYPE: PRT
 ; ORGANISM: Bos taurus

US-10-014-162-5

Query Match 89.7%; Score 35; DB 15; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.3e-25;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
 |||||
 Db 1 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 35

RESULT 11

US-10-014-162-41

; Sequence 41, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 41
 ; LENGTH: 35
 ; TYPE: PRT
 ; ORGANISM: Bos taurus

US-10-014-162-41

Query Match 89.7%; Score 35; DB 15; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.3e-25;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35
          |||||||||||||||||||||||||||||||||||
Db      1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35
```

RESULT 12

US-10-014-162-6

; Sequence 6, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Bos taurus

US-10-014-162-6

Query Match 87.2%; Score 34; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e-24;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      6 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
          |||||||||||||||||||||||||||||||||||
Db      1 DDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 34
```

RESULT 13

US-10-014-162-42

; Sequence 42, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42

; LENGTH: 34
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-42

Query Match 87.2%; Score 34; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e-24;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34
|||||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34

RESULT 14

US-10-014-162-7
; Sequence 7, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-7

Query Match 84.6%; Score 33; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 33

RESULT 15

US-10-014-162-43
; Sequence 43, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11


```
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-014-162-44
```

```
Query Match          82.1%; Score 32; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32
          |||
Db      1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32
```

RESULT 18

```
US-10-014-162-9
; Sequence 9, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-014-162-9
```

```
Query Match          79.5%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
          |||
```


Query Match 79.5%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 AFRERARLLAALERRHWLNSYMHKLLVLDAP 31

RESULT 21

US-10-014-162-10

; Sequence 10, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-10

Query Match 76.9%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 22

US-10-014-162-46

; Sequence 46, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15


```

; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 29
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-014-162-11

```

```

Query Match          74.4%;  Score 29;  DB 15;  Length 29;
Best Local Similarity 100.0%;  Pred. No. 1.3e-19;
Matches 29;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
          |||
Db      1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

```

RESULT 25

```

US-10-014-162-47
; Sequence 47, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 29
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-014-162-47

```

```

Query Match          74.4%;  Score 29;  DB 15;  Length 29;
Best Local Similarity 100.0%;  Pred. No. 1.3e-19;
Matches 29;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 SLALADDAAFRERARLLAALERRHWLNSY 29
          |||
Db      1 SLALADDAAFRERARLLAALERRHWLNSY 29

```

RESULT 26

US-10-014-162-80
; Sequence 80, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-80

Query Match 74.4%; Score 29; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 27

US-10-014-162-48
; Sequence 48, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-48

Query Match 71.8%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNS 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SLALADDAAFRERARLLAALERRHWLNS 28

RESULT 28

US-10-154-884B-11122

; Sequence 11122, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 11122

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-11122

Query Match 15.4%; Score 6; DB 12; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALERR 23
| | | | |

Db

3 AALERR 8

RESULT 29

US-10-154-884B-11106

; Sequence 11106, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 11106

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-11106

Query Match 15.4%; Score 6; DB 12; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALERR 23

|||||

Db 3 AALERR 8

RESULT 30

US-10-026-741-7

; Sequence 7, Application US/10026741

; Publication No. US20030049604A1

; GENERAL INFORMATION:

; APPLICANT: CHARNEAU, PIERRE
; CLAVEL, FRANCOISE
; BORMAN, ANDREW
; QUILLEN, CAROLINE
; GUETARD, DENISE
; MONTAGNIER, LUC
; DONJON DE SAINT-MARTIN, JACQUELINE
; COHEN, JAKUES

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
; SUBTYPE) ANTIGENS

; NUMBER OF SEQUENCES: 103

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/026,741

; FILING DATE: 27-Dec-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/817,441

; FILING DATE: 31-AUG-1998

; APPLICATION NUMBER: PCT/FR 95/01391

; FILING DATE: 20-OCT-1995

; APPLICATION NUMBER: FR 9412554

; FILING DATE: 20-OCT-1994

; APPLICATION NUMBER: FR 9502526

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03260.6005-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 37 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-026-741-7

Query Match 15.4%; Score 6; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 1 RARLLA 6

RESULT 31

US-09-779-451-40

; Sequence 40, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (18)..(18)
; OTHER INFORMATION: May be any amino acid
US-09-779-451-40

Query Match 15.4%; Score 6; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 25 RARLLA 30

RESULT 32

US-09-864-761-37845

; Sequence 37845, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37845
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031665.18
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EST_HUMAN HIT: AV709682.1, EVALUE 4.00e-03
US-09-864-761-37845

Query Match 12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RARLL 17
|||
Db 20 RARLL 24

RESULT 33

US-09-864-761-38197

; Sequence 38197, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38197
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL109809.14
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
;   OTHER INFORMATION: EST_HUMAN HIT: BE514786.1, EVALUE 2.70e-02
US-09-864-761-38197

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Query Match          12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      13 RARLL 17
        |||||
Db      13 RARLL 17

```

RESULT 34

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US-09-864-761-45958
; Sequence 45958, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45958
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL109809.18
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
;   OTHER INFORMATION: EST_HUMAN HIT: BE514786.1, EVALUE 4.00e-01
US-09-864-761-45958

```

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Query Match          12.8%;  Score 5;  DB 9;  Length 28;
Best Local Similarity 100.0%;  Pred. No. 8.9e+02;
Matches      5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      13 RARLL 17
        |||||
Db      15 RARLL 19

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RESULT 35
US-09-782-980-145
; Sequence 145, Application US/09782980

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; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-980-145

```

```

Query Match          12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

Db

|||||
7 LALAD 11

RESULT 36

US-09-776-724A-114

; Sequence 114, Application US/09776724A
; Publication No. US20030050455A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: PZ011
; CURRENT APPLICATION NUMBER: US/09/776,724A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,909
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/669,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,873
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724

; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-724A-114

Query Match 12.8%; Score 5; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
|||||
Db 7 KLLVL 11

RESULT 37

US-10-001-887-123

; Sequence 123, Application US/10001887

; Publication No. US20020155464A1

; GENERAL INFORMATION:

; APPLICANT: Salceda, Susana

; APPLICANT: Macina, Roberto

; APPLICANT: Recipon, Herve

; APPLICANT: Cafferkey, Robert

; APPLICANT: Sun, Yongming

; APPLICANT: Liu, Chenghua

; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
Genes and Proteins

; FILE REFERENCE: DEX-0269

; CURRENT APPLICATION NUMBER: US/10/001,887

; CURRENT FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/249,998

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: 60/252,563

; PRIOR FILING DATE: 2000-11-22

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 123

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-001-887-123

Query Match 12.8%; Score 5; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
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Db 8 KLLVL 12

RESULT 38

US-09-905-831-12

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; Sequence 12, Application US/09905831
; Patent No. US20020119572A1
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Joseph
; APPLICANT: Schwartz, John
; APPLICANT: Hamad, Kimberly
; APPLICANT: Zhang, Shuguang
; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides
; FILE REFERENCE: MLB-086
; CURRENT APPLICATION NUMBER: US/09/905,831
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/276,313
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/218,312
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dCoil-adIL29 dimeric coiled coil
US-09-905-831-12
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Query Match          12.8%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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Qy      17 LAAL 21
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Db      9 LAAL 13
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RESULT 39

US-09-905-831-14

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; Sequence 14, Application US/09905831
; Patent No. US20020119572A1
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Joseph
; APPLICANT: Schwartz, John
; APPLICANT: Hamad, Kimberly
; APPLICANT: Zhang, Shuguang
; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides
; FILE REFERENCE: MLB-086
; CURRENT APPLICATION NUMBER: US/09/905,831
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/276,313
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/218,312
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 14
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dCoil-LA29 dimeric coiled coil
US-09-905-831-14

Query Match 12.8%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
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Db 2 LAALE 6

RESULT 40

US-09-905-831-15
; Sequence 15, Application US/09905831
; Patent No. US20020119572A1
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Joseph
; APPLICANT: Schwartz, John
; APPLICANT: Hamad, Kimberly
; APPLICANT: Zhang, Shuguang
; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides
; FILE REFERENCE: MLB-086
; CURRENT APPLICATION NUMBER: US/09/905,831
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/276,313
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/218,312
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tCoil-LL29 trimeric bundle
US-09-905-831-15

Query Match 12.8%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
|||
Db 9 LAALE 13

Search completed: January 14, 2004, 11:15:12
Job time : 27.243 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 29.1589 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	6	15.4	37	16	Q8P6H8	Q8p6h8 xanthomonas
2	6	15.4	38	16	Q8FVK2	Q8fvk2 brucella su
3	5	12.8	28	5	Q9TWE2	Q9twe2 paracentrot
4	5	12.8	28	11	Q9WTS1	Q9wts1 rattus norv
5	5	12.8	29	6	Q9TTP2	Q9ttp2 pan troglod
6	5	12.8	29	11	Q9JLR6	Q9jlr6 rattus norv
7	5	12.8	29	16	Q9I390	Q9i390 pseudomonas
8	5	12.8	31	2	Q9RHF9	Q9rhf9 acinetobact
9	5	12.8	31	9	Q9T1K0	Q9t1k0 bacterioph
10	5	12.8	31	9	Q9T1K2	Q9t1k2 bacterioph
11	5	12.8	31	9	Q9T1K1	Q9t1k1 bacterioph
12	5	12.8	31	9	Q9T1K3	Q9t1k3 bacterioph
13	5	12.8	33	16	Q9KM83	Q9km83 vibrio chol
14	5	12.8	33	16	Q8XY48	Q8xy48 ralstonia s
15	5	12.8	37	5	Q27372	Q27372 bombyx mori
16	5	12.8	37	5	Q8SYH5	Q8syh5 drosophila
17	5	12.8	37	6	Q9TTR4	Q9ttr4 cercopithec
18	5	12.8	37	6	Q9N260	Q9n260 sus scrofa
19	5	12.8	38	4	Q9H4Y8	Q9h4y8 homo sapien
20	5	12.8	38	16	Q8U580	Q8u580 agrobacteri
21	5	12.8	39	2	Q9LB47	Q9lb47 helicobacte
22	5	12.8	39	4	Q9UDI2	Q9udi2 homo sapien
23	5	12.8	39	5	O61645	O61645 aplysia cal
24	5	12.8	39	9	Q9ZXX1	Q9zxx1 bacterioph
25	5	12.8	39	10	Q9ZRY5	Q9zry5 prunus aviu
26	5	12.8	39	15	Q9PXW1	Q9pxw1 simian immu
27	5	12.8	39	16	Q8F6J1	Q8f6j1 leptospira
28	4	10.3	28	4	Q8NHY1	Q8nhyl homo sapien
29	4	10.3	28	6	Q8MJG7	Q8mjb7 sus scrofa
30	4	10.3	28	6	Q95L33	Q95l33 equus cabal
31	4	10.3	28	8	P92760	P92760 uromastix a
32	4	10.3	28	11	Q9QVC9	Q9qvc9 rattus sp.
33	4	10.3	28	11	Q62677	Q62677 rattus norv
34	4	10.3	29	3	Q8TGQ9	Q8tgq9 saccharomyc
35	4	10.3	29	4	Q9BR24	Q9br24 homo sapien
36	4	10.3	29	4	Q9UBW6	Q9ubw6 homo sapien
37	4	10.3	29	4	Q9UCW5	Q9ucw5 homo sapien
38	4	10.3	29	5	Q9BM71	Q9bm71 lasius nige
39	4	10.3	29	7	Q29891	Q29891 homo sapien
40	4	10.3	29	7	O19668	O19668 homo sapien
41	4	10.3	29	7	Q30141	Q30141 homo sapien
42	4	10.3	29	7	O19735	O19735 homo sapien
43	4	10.3	29	7	Q29807	Q29807 homo sapien
44	4	10.3	29	7	O19733	O19733 homo sapien
45	4	10.3	29	7	Q29892	Q29892 homo sapien
46	4	10.3	29	7	O19661	O19661 homo sapien
47	4	10.3	29	7	O19663	O19663 homo sapien
48	4	10.3	29	7	O19737	O19737 homo sapien
49	4	10.3	29	7	O19665	O19665 homo sapien
50	4	10.3	29	7	Q29815	Q29815 homo sapien
51	4	10.3	29	7	O19734	O19734 homo sapien
52	4	10.3	29	7	O19662	O19662 homo sapien
53	4	10.3	29	7	Q30138	Q30138 homo sapien
54	4	10.3	29	7	O19731	O19731 homo sapien
55	4	10.3	29	7	O19681	O19681 homo sapien
56	4	10.3	29	7	O19666	O19666 homo sapien
57	4	10.3	29	7	Q30140	Q30140 homo sapien

58	4	10.3	29	7	Q06662	Q06662 homo sapien
59	4	10.3	29	7	Q06654	Q06654 homo sapien
60	4	10.3	29	7	Q06664	Q06664 homo sapien
61	4	10.3	29	7	Q29808	Q29808 homo sapien
62	4	10.3	29	7	Q06663	Q06663 homo sapien
63	4	10.3	29	8	Q9G651	Q9g651 otocryptis
64	4	10.3	29	11	Q9R1N7	Q9rln7 mus musculu
65	4	10.3	29	11	Q8VHI0	Q8vhi0 mus musculu
66	4	10.3	29	11	Q9JLQ6	Q9jllq6 rattus norv
67	4	10.3	29	11	Q9WVC4	Q9wvc4 mus musculu
68	4	10.3	29	16	Q8CLI6	Q8cli6 yersinia pe
69	4	10.3	30	2	Q9R4Z7	Q9r4z7 neisseria c
70	4	10.3	30	2	Q9R5C4	Q9r5c4 comamonas.
71	4	10.3	30	2	Q9R4N4	Q9r4n4 staphylococ
72	4	10.3	30	2	O85590	O85590 chlamydia t
73	4	10.3	30	4	Q96EU1	Q96eul homo sapien
74	4	10.3	30	4	Q15980	Q15980 homo sapien
75	4	10.3	30	5	Q95P86	Q95p86 mesobuthus
76	4	10.3	30	6	Q8MHW1	Q8mhw1 sus scrofa
77	4	10.3	30	7	Q31234	Q31234 mus musculu
78	4	10.3	30	10	Q9SJL3	Q9sjl3 arabidopsis
79	4	10.3	30	11	Q9QV95	Q9qv95 cavia (guin
80	4	10.3	30	11	Q9QV42	Q9qv42 rattus sp.
81	4	10.3	30	12	P89878	P89878 molluscum c
82	4	10.3	30	16	Q8VJU1	Q8vjul mycobacteri
83	4	10.3	30	16	Q8G2I8	Q8g2i8 brucella su
84	4	10.3	31	2	Q9S5Z5	Q9s5z5 streptomyce
85	4	10.3	31	2	Q9JP49	Q9jp49 azospirillu
86	4	10.3	31	2	Q9L7N7	Q9l7n7 borrelia af
87	4	10.3	31	2	Q9KWY1	Q9kwy1 streptococc
88	4	10.3	31	4	Q9NYP6	Q9nyp6 homo sapien
89	4	10.3	31	6	O77625	O77625 bos taurus
90	4	10.3	31	6	Q95M83	Q95m83 equus cabal
91	4	10.3	31	10	Q9S8M6	Q9s8m6 lupinus alb
92	4	10.3	31	10	Q9FUQ2	Q9fuq2 zea mays (s
93	4	10.3	31	11	Q60419	Q60419 cricetulus
94	4	10.3	31	13	Q91705	Q91705 xenopus lae
95	4	10.3	31	13	Q9W7F4	Q9w7f4 labeo rohit
96	4	10.3	31	16	Q9PGM7	Q9pgm7 xylella fas
97	4	10.3	31	16	Q8U5T3	Q8u5t3 agrobacteri
98	4	10.3	31	16	Q8VJ21	Q8vj21 mycobacteri
99	4	10.3	31	16	Q8VJ13	Q8vj13 mycobacteri
100	4	10.3	31	16	P74787	P74787 synechocyst
101	4	10.3	31	16	Q8NW38	Q8nw38 staphylococ
102	4	10.3	31	16	Q8E895	Q8e895 shewanella
103	4	10.3	32	2	Q44499	Q44499 anabaena va
104	4	10.3	32	3	P78708	P78708 neurospora
105	4	10.3	32	4	Q96RX4	Q96rx4 homo sapien
106	4	10.3	32	6	Q9BEF6	Q9bef6 capra hircu
107	4	10.3	32	8	Q8SL89	Q8sl89 euglena ste
108	4	10.3	32	8	Q9MS54	Q9ms54 euglena vir
109	4	10.3	32	10	Q9FUQ3	Q9fuq3 zea mays (s
110	4	10.3	32	10	Q9FE82	Q9fe82 zea mays (s
111	4	10.3	32	10	Q9FE81	Q9fe81 zea mays (s
112	4	10.3	32	10	Q9FUQ1	Q9fuq1 zea mays (s
113	4	10.3	32	10	Q9FUQ5	Q9fuq5 zea mays su
114	4	10.3	32	10	Q9FUP9	Q9fup9 zea luxuria

115	4	10.3	32	10	Q9FUQ4	Q9fuq4	zea	mays	(s
116	4	10.3	32	10	Q9FUQ0	Q9fuq0	zea	luxuria	
117	4	10.3	32	10	Q9FE80	Q9fe80	zea	diplope	
118	4	10.3	32	10	Q9FUP8	Q9fup8	zea	luxuria	
119	4	10.3	32	11	Q9JIU1	Q9jiu1	rattus	norv	
120	4	10.3	32	11	Q9R1C2	Q9rlc2	mus	musculu	
121	4	10.3	32	13	O57364	O57364	brachydanio		
122	4	10.3	32	13	Q9YGR4	Q9ygr4	gallus	gall	
123	4	10.3	32	16	Q932N6	Q932n6	staphylococ		
124	4	10.3	32	16	Q8VJ76	Q8vj76	mycobacteri		
125	4	10.3	32	16	Q9K4G0	Q9k4g0	streptomyce		
126	4	10.3	32	16	Q8EJG9	Q8ejg9	shewanella		
127	4	10.3	32	16	Q8EBJ9	Q8ebj9	shewanella		
128	4	10.3	32	17	Q9HNL3	Q9hnl3	halobacteri		
129	4	10.3	33	2	O30547	O30547	pseudomonas		
130	4	10.3	33	2	Q45283	Q45283	bacillus	li	
131	4	10.3	33	4	Q8IZ90	Q8iz90	homo	sapien	
132	4	10.3	33	8	Q9MS60	Q9ms60	euglena	san	
133	4	10.3	33	8	Q9MS57	Q9ms57	euglena	ste	
134	4	10.3	33	8	Q8HUN2	Q8hun2	populus	tom	
135	4	10.3	33	12	O11372	O11372	molluscum	c	
136	4	10.3	33	13	Q9PS28	Q9ps28	cerastes	ce	
137	4	10.3	33	16	Q9KTZ5	Q9ktz5	vibrio	chol	
138	4	10.3	33	16	Q97RJ3	Q97rj3	streptococc		
139	4	10.3	33	16	Q932N2	Q932n2	staphylococ		
140	4	10.3	33	16	Q8U5P2	Q8u5p2	agrobacteri		
141	4	10.3	33	16	Q8VJZ2	Q8vjz2	mycobacteri		
142	4	10.3	33	16	Q8P8K6	Q8p8k6	xanthomonas		
143	4	10.3	33	16	Q8G114	Q8gl14	brucella	su	
144	4	10.3	33	16	Q8FY86	Q8fy86	brucella	su	
145	4	10.3	33	16	Q8EBD6	Q8ebd6	shewanella		
146	4	10.3	33	16	Q8CQY7	Q8cqy7	staphylococ		
147	4	10.3	33	16	Q8CLN5	Q8cln5	yersinia	pe	
148	4	10.3	33	17	Q8ZY37	Q8zy37	pyrobaculum		
149	4	10.3	34	2	Q9Z4Q3	Q9z4q3	corynebacte		
150	4	10.3	34	2	Q9S3W3	Q9s3w3	mastigoclad		
151	4	10.3	34	2	Q9RE23	Q9re23	helicobacte		
152	4	10.3	34	4	Q9UI64	Q9ui64	homo	sapien	
153	4	10.3	34	4	Q96IX0	Q96ix0	homo	sapien	
154	4	10.3	34	4	Q96J93	Q96j93	homo	sapien	
155	4	10.3	34	5	Q8T3M2	Q8t3m2	drosophila		
156	4	10.3	34	8	Q9GI95	Q9gi95	sargassum	s	
157	4	10.3	34	8	Q32752	Q32752	oryza	sativ	
158	4	10.3	34	11	Q925F8	Q925f8	rattus	norv	
159	4	10.3	34	11	Q8VHL4	Q8vhl4	rattus	norv	
160	4	10.3	34	12	Q9E8K5	Q9e8k5	hepatitis	b	
161	4	10.3	34	16	Q8EHU5	Q8ehu5	shewanella		
162	4	10.3	34	16	Q8CLQ6	Q8clq6	yersinia	pe	
163	4	10.3	34	17	Q9HMS8	Q9hms8	halobacteri		
164	4	10.3	35	2	Q9RE20	Q9re20	helicobacte		
165	4	10.3	35	2	Q9RE26	Q9re26	helicobacte		
166	4	10.3	35	2	Q53272	Q53272	escherichia		
167	4	10.3	35	2	Q9RE21	Q9re21	helicobacte		
168	4	10.3	35	2	Q9R2Y4	Q9r2y4	helicobacte		
169	4	10.3	35	2	Q9RE27	Q9re27	helicobacte		
170	4	10.3	35	2	Q51963	Q51963	pseudomonas		
171	4	10.3	35	2	O53109	O53109	mycoplasma		

172	4	10.3	35	2	Q8KM41	Q8km41 mycobacteri
173	4	10.3	35	2	Q9RE24	Q9re24 helicobacte
174	4	10.3	35	2	Q9RE25	Q9re25 helicobacte
175	4	10.3	35	2	Q9R2Y5	Q9r2y5 helicobacte
176	4	10.3	35	2	Q8VT19	Q8vt19 enterococcu
177	4	10.3	35	2	Q9R2Y6	Q9r2y6 helicobacte
178	4	10.3	35	2	Q9RE22	Q9re22 helicobacte
179	4	10.3	35	3	Q14374	Q14374 schizosacch
180	4	10.3	35	4	Q96RX9	Q96rx9 homo sapien
181	4	10.3	35	4	Q9UED0	Q9ued0 homo sapien
182	4	10.3	35	5	Q9GTB7	Q9gtb7 neospora ca
183	4	10.3	35	10	Q8GUX3	Q8gux3 picea maria
184	4	10.3	35	13	Q09133	Q09133 xenopus lae
185	4	10.3	35	15	Q8UT29	Q8ut29 human immun
186	4	10.3	35	16	Q9PPG6	Q9ppg6 campylobact
187	4	10.3	35	16	Q8Z0F9	Q8z0f9 anabaena sp
188	4	10.3	35	16	Q8U5A2	Q8u5a2 agrobacteri
189	4	10.3	35	16	Q8VKN5	Q8vkn5 mycobacteri
190	4	10.3	36	2	O53108	O53108 mycoplasma
191	4	10.3	36	2	Q44153	Q44153 actinobacil
192	4	10.3	36	4	Q96G89	Q96g89 homo sapien
193	4	10.3	36	4	Q9UI80	Q9ui80 homo sapien
194	4	10.3	36	6	Q8SPM7	Q8spm7 canis famil
195	4	10.3	36	8	O79185	O79185 ninox rufa.
196	4	10.3	36	10	Q8W502	Q8w502 dichelostem
197	4	10.3	36	11	Q920Z5	Q920z5 rattus sp.
198	4	10.3	36	16	O50686	O50686 borrelia bu
199	4	10.3	36	16	Q9A5R6	Q9a5r6 caulobacter
200	4	10.3	36	16	Q8PK38	Q8pk38 xanthomonas
201	4	10.3	36	16	Q8EYJ2	Q8eyj2 leptospira
202	4	10.3	36	16	Q8EC61	Q8ec61 shewanella
203	4	10.3	36	16	Q8EBV5	Q8ebv5 shewanella
204	4	10.3	37	4	Q9BW21	Q9bw21 homo sapien
205	4	10.3	37	4	Q8TD81	Q8td81 homo sapien
206	4	10.3	37	4	Q96HV0	Q96hv0 homo sapien
207	4	10.3	37	5	Q17245	Q17245 bombyx mori
208	4	10.3	37	5	Q17244	Q17244 bombyx mori
209	4	10.3	37	5	Q8MPH4	Q8mph4 schistosoma
210	4	10.3	37	9	Q8HAH3	Q8hah3 salmonella
211	4	10.3	37	10	Q9S8D8	Q9s8d8 malus domes
212	4	10.3	37	11	Q8BMY3	Q8bmy3 mus musculu
213	4	10.3	37	12	Q98151	Q98151 kaposi's sa
214	4	10.3	37	12	Q8AYZ0	Q8ayz0 goose circo
215	4	10.3	37	12	Q8AYY4	Q8ayy4 goose circo
216	4	10.3	37	13	Q9PRK6	Q9prk6 gallus sp.
217	4	10.3	37	13	O57376	O57376 brachydanio
218	4	10.3	37	13	Q9PRK1	Q9prk1 gallus sp.
219	4	10.3	37	16	Q9X089	Q9x089 thermotoga
220	4	10.3	37	16	Q9KPZ4	Q9kpz4 vibrio chol
221	4	10.3	37	16	Q9KEJ6	Q9kej6 bacillus ha
222	4	10.3	37	16	Q8KD28	Q8kd28 chlorobium
223	4	10.3	37	16	Q8FVV0	Q8fvv0 brucella su
224	4	10.3	37	16	Q8EIQ2	Q8eiq2 shewanella
225	4	10.3	37	17	Q9HRW1	Q9hrw1 halobacteri
226	4	10.3	38	2	Q9F5C7	Q9f5c7 agrobacteri
227	4	10.3	38	2	Q9R7M2	Q9r7m2 escherichia
228	4	10.3	38	2	Q8KYC9	Q8kyc9 bacillus an

229	4	10.3	38	2	Q939W1	Q939w1 aeromonas s
230	4	10.3	38	2	Q8GNN7	Q8gnn7 escherichia
231	4	10.3	38	4	Q8TDB1	Q8tdb1 homo sapien
232	4	10.3	38	4	Q8IZ88	Q8iz88 homo sapien
233	4	10.3	38	5	O96617	O96617 echinococcu
234	4	10.3	38	11	Q91XM1	Q91xm1 rattus norv
235	4	10.3	38	13	Q9PTV6	Q9ptv6 oryzias lat
236	4	10.3	38	13	Q9PTV7	Q9ptv7 oryzias lat
237	4	10.3	38	15	O55472	O55472 human immun
238	4	10.3	38	16	Q9KLC0	Q9klc0 vibrio chol
239	4	10.3	38	17	Q8ZX52	Q8zx52 pyrobaculum
240	4	10.3	39	4	Q9NQQ8	Q9nqq8 homo sapien
241	4	10.3	39	4	Q9UD56	Q9ud56 homo sapien
242	4	10.3	39	4	Q9UD60	Q9ud60 homo sapien
243	4	10.3	39	4	Q9UC03	Q9uc03 homo sapien
244	4	10.3	39	5	Q23904	Q23904 dictyosteli
245	4	10.3	39	5	Q9V8G0	Q9v8g0 drosophila
246	4	10.3	39	8	Q9XLU0	Q9xlu0 saccharomyc
247	4	10.3	39	8	Q36197	Q36197 ursus arcto
248	4	10.3	39	12	Q9IW57	Q9iw57 borna disea
249	4	10.3	39	13	O73604	O73604 gallus gall
250	4	10.3	39	16	Q9PFD3	Q9pfd3 xylella fas
251	4	10.3	39	16	Q9KM79	Q9km79 vibrio chol
252	4	10.3	39	16	Q9A7N6	Q9a7n6 caulobacter
253	4	10.3	39	16	Q8ZK28	Q8zk28 salmonella
254	4	10.3	39	16	Q8X406	Q8x406 escherichia
255	4	10.3	39	16	Q8VK19	Q8vk19 mycobacteri
256	4	10.3	39	16	Q9KXN7	Q9kxn7 streptomyce
257	4	10.3	39	16	Q8DXQ2	Q8dxq2 streptococc
258	4	10.3	40	2	Q55331	Q55331 synechocyst
259	4	10.3	40	2	O69584	O69584 mycobacteri
260	4	10.3	40	3	Q9URF6	Q9urf6 saccharomyc
261	4	10.3	40	4	Q8WYE5	Q8wye5 homo sapien
262	4	10.3	40	5	Q9UAF4	Q9uaf4 halocynthia
263	4	10.3	40	5	Q8IME0	Q8ime0 drosophila
264	4	10.3	40	7	Q9TNZ4	Q9tnz4 rattus norv
265	4	10.3	40	8	Q05333	Q05333 petunia sp.
266	4	10.3	40	8	Q8MFP6	Q8mfp6 vitis vinif
267	4	10.3	40	10	Q8S5P4	Q8s5p4 oryza sativ
268	4	10.3	40	11	Q923H1	Q923h1 cricetulus
269	4	10.3	40	13	Q9PRT5	Q9prt5 rana catesb
270	4	10.3	40	16	O24910	O24910 helicobacte
271	4	10.3	40	16	Q9I1X6	Q9ilx6 pseudomonas
272	4	10.3	40	16	Q935Q4	Q935q4 salmonella
273	4	10.3	40	16	Q8KE46	Q8ke46 chlorobium
274	4	10.3	40	16	Q8EYM7	Q8eym7 leptospira
275	4	10.3	40	16	Q8EXS6	Q8exs6 leptospira
276	4	10.3	40	16	Q8EGK3	Q8egk3 shewanella
277	3	7.7	28	1	Q9UWI5	Q9uwi5 archaeoglob
278	3	7.7	28	1	Q9UWL1	Q9uwl1 pyrococcus
279	3	7.7	28	2	Q47565	Q47565 escherichia
280	3	7.7	28	2	Q47354	Q47354 escherichia
281	3	7.7	28	2	Q47372	Q47372 escherichia
282	3	7.7	28	2	Q47373	Q47373 escherichia
283	3	7.7	28	2	Q9R4Z1	Q9r4z1 chloroflexu
284	3	7.7	28	2	Q47368	Q47368 escherichia
285	3	7.7	28	2	Q47359	Q47359 escherichia

286	3	7.7	28	2	Q47371	Q47371	escherichia
287	3	7.7	28	2	Q47358	Q47358	escherichia
288	3	7.7	28	2	Q9R5I4	Q9r5i4	streptococc
289	3	7.7	28	2	Q47365	Q47365	escherichia
290	3	7.7	28	2	Q47370	Q47370	escherichia
291	3	7.7	28	2	Q9R4G6	Q9r4g6	eubacterium
292	3	7.7	28	2	Q52275	Q52275	pseudomonas
293	3	7.7	28	2	Q9F7C1	Q9f7c1	serratia ma
294	3	7.7	28	2	Q47352	Q47352	escherichia
295	3	7.7	28	2	Q47736	Q47736	enterococcu
296	3	7.7	28	2	Q47357	Q47357	escherichia
297	3	7.7	28	2	Q49327	Q49327	mycoplasma
298	3	7.7	28	2	Q9R5E6	Q9r5e6	thermus aqu
299	3	7.7	28	2	Q47369	Q47369	escherichia
300	3	7.7	28	2	Q9REI4	Q9rei4	acidiphiliu
301	3	7.7	28	2	Q9R4L5	Q9r4l5	helicobacte
302	3	7.7	28	2	Q47360	Q47360	escherichia
303	3	7.7	28	2	Q47366	Q47366	escherichia
304	3	7.7	28	2	Q52623	Q52623	proteus vul
305	3	7.7	28	2	Q47367	Q47367	escherichia
306	3	7.7	28	2	Q46752	Q46752	escherichia
307	3	7.7	28	2	Q9R5C7	Q9r5c7	vibrio para
308	3	7.7	28	2	Q08005	Q08005	lactococcus
309	3	7.7	28	2	Q47356	Q47356	escherichia
310	3	7.7	28	2	Q93JY6	Q93jy6	mycobacteri
311	3	7.7	28	2	Q47363	Q47363	escherichia
312	3	7.7	28	2	Q93KE4	Q93ke4	chlamydia p
313	3	7.7	28	2	Q9R4X0	Q9r4x0	synechococc
314	3	7.7	28	2	Q9ZB83	Q9zb83	vibrio angu
315	3	7.7	28	3	P87021	P87021	magnaporthe
316	3	7.7	28	3	Q00440	Q00440	glomerella
317	3	7.7	28	4	Q8N670	Q8n670	homo sapien
318	3	7.7	28	4	Q8N2V3	Q8n2v3	homo sapien
319	3	7.7	28	4	O43804	O43804	homo sapien
320	3	7.7	28	4	Q9UD92	Q9ud92	homo sapien
321	3	7.7	28	4	Q9H4R8	Q9h4r8	homo sapien
322	3	7.7	28	4	Q8WUY6	Q8wuy6	homo sapien
323	3	7.7	28	4	Q8NG21	Q8ng21	homo sapien
324	3	7.7	28	4	Q16325	Q16325	homo sapien
325	3	7.7	28	4	Q9UMB1	Q9umb1	homo sapien
326	3	7.7	28	4	Q15839	Q15839	homo sapien
327	3	7.7	28	4	Q9HB33	Q9hb33	homo sapien
328	3	7.7	28	4	Q9NQR3	Q9nqr3	homo sapien
329	3	7.7	28	4	Q8J018	Q8j018	homo sapien
330	3	7.7	28	4	Q8IZT7	Q8izt7	homo sapien
331	3	7.7	28	4	Q8IZL0	Q8izl0	homo sapien
332	3	7.7	28	4	Q8IZK3	Q8izk3	homo sapien
333	3	7.7	28	4	Q8IZK2	Q8izk2	homo sapien
334	3	7.7	28	4	Q8IZ87	Q8iz87	homo sapien
335	3	7.7	28	5	Q9BM57	Q9bm57	lineus sp.
336	3	7.7	28	5	Q9BM76	Q9bm76	giardia lam
337	3	7.7	28	5	Q9BM74	Q9bm74	giardia lam
338	3	7.7	28	5	Q9TWT9	Q9twt9	penaeus jap
339	3	7.7	28	5	Q95NM7	Q95nm7	lithobius f
340	3	7.7	28	5	Q9GPK8	Q9gpk8	scutigere
341	3	7.7	28	5	Q9BM75	Q9bm75	giardia lam
342	3	7.7	28	6	Q9TRM4	Q9trm4	bos taurus

343	3	7.7	28	6	O62731	O62731	canis famil
344	3	7.7	28	6	Q9TRV2	Q9trv2	canis famil
345	3	7.7	28	6	Q9XS67	Q9xs67	bos taurus
346	3	7.7	28	6	Q9TU57	Q9tu57	papio cynoc
347	3	7.7	28	6	O62821	O62821	bubalus bub
348	3	7.7	28	6	Q9TU56	Q9tu56	colobus gue
349	3	7.7	28	6	Q9TU58	Q9tu58	trachypithe
350	3	7.7	28	6	Q8WP02	Q8wp02	ateles belz
351	3	7.7	28	7	O19736	O19736	homo sapien
352	3	7.7	28	7	O19732	O19732	homo sapien
353	3	7.7	28	8	Q8WK64	Q8wk64	pinus leiop
354	3	7.7	28	8	Q8WK92	Q8wk92	pinus carib
355	3	7.7	28	8	Q8WK52	Q8wk52	pinus herre
356	3	7.7	28	8	Q8WK78	Q8wk78	pinus palus
357	3	7.7	28	8	Q8WK60	Q8wk60	pinus oocar
358	3	7.7	28	8	Q8WK44	Q8wk44	pinus roxbu
359	3	7.7	28	8	Q8WK48	Q8wk48	pinus dougl
360	3	7.7	28	8	Q8WK94	Q8wk94	pinus atten
361	3	7.7	28	8	Q8WK66	Q8wk66	pinus virgi
362	3	7.7	28	8	Q8WK74	Q8wk74	pinus punge
363	3	7.7	28	8	Q8WK70	Q8wk70	pinus taeda
364	3	7.7	28	8	Q8WK54	Q8wk54	pinus carib
365	3	7.7	28	8	Q9Zyv5	Q9zyv5	dipsosaurus
366	3	7.7	28	8	Q9T2U2	Q9t2u2	bos taurus
367	3	7.7	28	8	Q33554	Q33554	crithidia f
368	3	7.7	28	8	Q8WK50	Q8wk50	pinus muric
369	3	7.7	28	8	Q37005	Q37005	oryza sativ
370	3	7.7	28	8	Q8WK72	Q8wk72	pinus rigid
371	3	7.7	28	8	Q9G5Y8	Q9g5y8	agama agama
372	3	7.7	28	8	Q8WK86	Q8wk86	pinus conto
373	3	7.7	28	8	Q8WK62	Q8wk62	pinus patul
374	3	7.7	28	8	Q8WK84	Q8wk84	pinus cuben
375	3	7.7	28	8	Q8WK88	Q8wk88	pinus carib
376	3	7.7	28	8	Q8WK82	Q8wk82	pinus maest
377	3	7.7	28	8	Q8WK58	Q8wk58	pinus radia
378	3	7.7	28	8	Q8WK80	Q8wk80	pinus mugo.
379	3	7.7	28	8	Q8WK56	Q8wk56	pinus resin
380	3	7.7	28	8	Q8WK90	Q8wk90	pinus banks
381	3	7.7	28	8	Q8LVZ6	Q8lvz6	astyanax al
382	3	7.7	28	8	Q8WK76	Q8wk76	pinus ponde
383	3	7.7	28	8	Q8MAY2	Q8may2	porana pani
384	3	7.7	28	8	Q8WK68	Q8wk68	pinus tropi
385	3	7.7	28	8	Q8HS23	Q8hs23	pisum sativ
386	3	7.7	28	8	Q8HS11	Q8hs11	spathiphyll
387	3	7.7	28	8	Q8HS07	Q8hs07	welwitschia
388	3	7.7	28	8	Q8HQU4	Q8hqu4	pinus jeffr
389	3	7.7	28	8	Q8HQU2	Q8hqu2	pinus engel
390	3	7.7	28	8	Q8HQR7	Q8hqr7	pinus ellio
391	3	7.7	28	8	Q8HQR5	Q8hqr5	pinus serot
392	3	7.7	28	8	Q8HQR3	Q8hqr3	pinus echin
393	3	7.7	28	10	Q8S6H4	Q8s6h4	oryza sativ
394	3	7.7	28	10	Q9XGH2	Q9xgh2	pisum sativ
395	3	7.7	28	10	Q9SAR3	Q9sar3	solanum tub
396	3	7.7	28	10	Q9XGE3	Q9xge3	vicia faba
397	3	7.7	28	10	O24218	O24218	oryza sativ
398	3	7.7	28	10	Q9XGE4	Q9xge4	vicia faba
399	3	7.7	28	10	Q41098	Q41098	populus bal

400	3	7.7	28	11	Q99PC4	Q99pc4	mus musculu
401	3	7.7	28	11	Q91XP0	Q91xp0	rattus norv
402	3	7.7	28	11	Q9EQ26	Q9eq26	mus musculu
403	3	7.7	28	11	Q91VP0	Q91vp0	mus musculu
404	3	7.7	28	12	Q67747	Q67747	human adeno
405	3	7.7	28	12	Q67782	Q67782	human adeno
406	3	7.7	28	12	Q67778	Q67778	human adeno
407	3	7.7	28	12	Q67781	Q67781	human adeno
408	3	7.7	28	12	Q67787	Q67787	human adeno
409	3	7.7	28	12	Q67754	Q67754	human adeno
410	3	7.7	28	12	Q67780	Q67780	human adeno
411	3	7.7	28	12	Q67756	Q67756	human adeno
412	3	7.7	28	12	Q67777	Q67777	human adeno
413	3	7.7	28	12	Q9QC16	Q9qc16	hepatitis c
414	3	7.7	28	12	Q67773	Q67773	human adeno
415	3	7.7	28	12	Q67769	Q67769	human adeno
416	3	7.7	28	12	Q67767	Q67767	human adeno
417	3	7.7	28	12	Q67761	Q67761	human adeno
418	3	7.7	28	12	Q67783	Q67783	human adeno
419	3	7.7	28	12	Q67757	Q67757	human adeno
420	3	7.7	28	12	Q9QC46	Q9qc46	hepatitis c
421	3	7.7	28	12	Q67764	Q67764	human adeno
422	3	7.7	28	12	Q9QC19	Q9qc19	hepatitis c
423	3	7.7	28	12	Q67755	Q67755	human adeno
424	3	7.7	28	12	Q67762	Q67762	human adeno
425	3	7.7	28	12	Q67784	Q67784	human adeno
426	3	7.7	28	12	Q67763	Q67763	human adeno
427	3	7.7	28	12	Q9QC14	Q9qc14	hepatitis c
428	3	7.7	28	12	Q67772	Q67772	human adeno
429	3	7.7	28	12	Q98130	Q98130	kaposi's sa
430	3	7.7	28	12	Q9QC24	Q9qc24	hepatitis c
431	3	7.7	28	12	Q67765	Q67765	human adeno
432	3	7.7	28	12	Q67766	Q67766	human adeno
433	3	7.7	28	12	Q67776	Q67776	human adeno
434	3	7.7	28	12	Q67775	Q67775	human adeno
435	3	7.7	28	12	Q9QC17	Q9qc17	hepatitis c
436	3	7.7	28	12	Q67774	Q67774	human adeno
437	3	7.7	28	12	Q67745	Q67745	human adeno
438	3	7.7	28	12	Q67758	Q67758	human adeno
439	3	7.7	28	12	Q67760	Q67760	human adeno
440	3	7.7	28	12	Q67771	Q67771	human adeno
441	3	7.7	28	12	Q83181	Q83181	cauliflower
442	3	7.7	28	12	Q67752	Q67752	human adeno
443	3	7.7	28	12	Q68009	Q68009	hepatitis b
444	3	7.7	28	12	Q68552	Q68552	hepatitis c
445	3	7.7	28	12	Q67753	Q67753	human adeno
446	3	7.7	28	12	Q67751	Q67751	human adeno
447	3	7.7	28	12	Q67770	Q67770	human adeno
448	3	7.7	28	12	Q67779	Q67779	human adeno
449	3	7.7	28	12	Q67750	Q67750	human adeno
450	3	7.7	28	12	Q67748	Q67748	human adeno
451	3	7.7	28	12	Q67768	Q67768	human adeno
452	3	7.7	28	12	Q9QC18	Q9qc18	hepatitis c
453	3	7.7	28	12	Q86649	Q86649	murine hepa
454	3	7.7	28	12	Q67785	Q67785	human adeno
455	3	7.7	28	12	Q9QC35	Q9qc35	hepatitis c
456	3	7.7	28	12	Q67746	Q67746	human adeno

457	3	7.7	28	12	Q67749	Q67749 human adeno
458	3	7.7	28	12	Q67759	Q67759 human adeno
459	3	7.7	28	13	Q9DD70	Q9dd70 gallus gall
460	3	7.7	28	13	Q90757	Q90757 gallus gall
461	3	7.7	28	13	Q9PRN9	Q9prn9 carassius a
462	3	7.7	28	13	Q9YH39	Q9yh39 xiphophorus
463	3	7.7	28	13	Q9PRI9	Q9pri9 amia calva
464	3	7.7	28	13	Q9PRN8	Q9prn8 carassius a
465	3	7.7	28	13	Q90W61	Q90w61 xenopus lae
466	3	7.7	28	13	Q9PRX4	Q9prx4 xenopus lae
467	3	7.7	28	13	Q8QFT6	Q8qft6 gallus gall
468	3	7.7	28	15	O71346	O71346 human endog
469	3	7.7	28	15	P89161	P89161 chimpanzee
470	3	7.7	28	15	Q72263	Q72263 human immun
471	3	7.7	28	16	Q9KDN3	Q9kdn3 bacillus ha
472	3	7.7	28	16	Q9KDN2	Q9kdn2 bacillus ha
473	3	7.7	28	16	Q9K9U0	Q9k9u0 bacillus ha
474	3	7.7	28	16	Q8Y051	Q8y051 ralstonia s
475	3	7.7	28	16	Q8X415	Q8x415 escherichia
476	3	7.7	28	16	Q8PB05	Q8pb05 xanthomonas
477	3	7.7	28	16	Q8E014	Q8e014 streptococc
478	3	7.7	28	16	Q8CLV6	Q8clv6 yersinia pe
479	3	7.7	28	16	Q8CKG3	Q8ckg3 yersinia pe
480	3	7.7	29	2	Q9ZG52	Q9zg52 chlamydia t
481	3	7.7	29	2	Q54200	Q54200 streptomyce
482	3	7.7	29	2	Q9L928	Q9l928 shigella so
483	3	7.7	29	2	Q9X3E3	Q9x3e3 prochloroco
484	3	7.7	29	2	Q9S3J5	Q9s3j5 escherichia
485	3	7.7	29	2	Q47633	Q47633 escherichia
486	3	7.7	29	2	Q9L926	Q9l926 shigella fl
487	3	7.7	29	2	Q9AKV1	Q9akv1 neisseria g
488	3	7.7	29	2	Q9R9K0	Q9r9k0 paracoccus
489	3	7.7	29	2	Q9R511	Q9r511 bacillus su
490	3	7.7	29	2	Q59396	Q59396 escherichia
491	3	7.7	29	2	Q938P6	Q938p6 borrelia bu
492	3	7.7	29	2	Q9R4B7	Q9r4b7 streptomyce
493	3	7.7	29	2	Q9L924	Q9l924 shigella bo
494	3	7.7	29	2	Q9F7A0	Q9f7a0 salmonella
495	3	7.7	29	2	Q9R5G9	Q9r5g9 rhodococcus
496	3	7.7	29	2	Q51692	Q51692 paracoccus
497	3	7.7	29	2	Q47389	Q47389 escherichia
498	3	7.7	29	2	Q8VV94	Q8vv94 marine psyc
499	3	7.7	29	2	Q9R5M6	Q9r5m6 streptomyce
500	3	7.7	29	3	Q9HDQ2	Q9hdq2 candida rug
501	3	7.7	29	3	P78747	P78747 saccharomyc
502	3	7.7	29	3	Q9UR77	Q9ur77 candida alb
503	3	7.7	29	4	Q8WVE2	Q8wve2 homo sapien
504	3	7.7	29	4	Q9UM98	Q9um98 homo sapien
505	3	7.7	29	4	Q9P2A1	Q9p2a1 homo sapien
506	3	7.7	29	4	Q9UCR6	Q9ucr6 homo sapien
507	3	7.7	29	4	Q9UM88	Q9um88 homo sapien
508	3	7.7	29	4	Q9UGJ6	Q9ugj6 homo sapien
509	3	7.7	29	4	Q8N2Z7	Q8n2z7 homo sapien
510	3	7.7	29	4	Q9UKX9	Q9ukx9 homo sapien
511	3	7.7	29	4	Q9UN87	Q9un87 homo sapien
512	3	7.7	29	4	Q8NEF6	Q8nef6 homo sapien
513	3	7.7	29	4	O43807	O43807 homo sapien

514	3	7.7	29	4	Q9UCL2	Q9ucl2	homo sapien
515	3	7.7	29	4	Q96FP2	Q96fp2	homo sapien
516	3	7.7	29	4	Q9BX18	Q9bx18	homo sapien
517	3	7.7	29	4	Q9BV72	Q9bv72	homo sapien
518	3	7.7	29	4	Q9Y447	Q9y447	homo sapien
519	3	7.7	29	4	Q9BYJ8	Q9byj8	homo sapien
520	3	7.7	29	5	Q9TWN8	Q9twn8	pseudaletia
521	3	7.7	29	5	Q8T3E8	Q8t3e8	caenorhabdi
522	3	7.7	29	5	Q9TWS4	Q9tws4	hirudinaria
523	3	7.7	29	5	Q26819	Q26819	trypanosoma
524	3	7.7	29	5	Q17073	Q17073	antheraea p
525	3	7.7	29	5	Q967U4	Q967u4	schistocerc
526	3	7.7	29	5	Q9GU41	Q9gu41	sycon rapha
527	3	7.7	29	5	Q95SA8	Q95sa8	drosophila
528	3	7.7	29	5	Q967U5	Q967u5	schistocerc
529	3	7.7	29	5	Q27301	Q27301	drosophila
530	3	7.7	29	5	Q8ITD6	Q8itd6	schistosoma
531	3	7.7	29	6	Q9TSS7	Q9tss7	felis silve
532	3	7.7	29	6	Q8WP11	Q8wp11	ateles belz
533	3	7.7	29	6	Q95LA5	Q95la5	macaca mula
534	3	7.7	29	6	Q9TU60	Q9tu60	gorilla gor
535	3	7.7	29	6	Q9MZW8	Q9mzw8	pongo pygma
536	3	7.7	29	6	Q9TU63	Q9tu63	pan paniscu
537	3	7.7	29	6	Q9TU62	Q9tu62	pan troglod
538	3	7.7	29	6	Q9N1W3	Q9nlw3	equus cabal
539	3	7.7	29	6	Q9TS04	Q9ts04	bos taurus
540	3	7.7	29	7	Q9TPN3	Q9tpn3	agelaius ph
541	3	7.7	29	7	Q9TPN0	Q9tpn0	agelaius ph
542	3	7.7	29	7	Q9XRK6	Q9xrk6	agelaius ph
543	3	7.7	29	7	Q9TPM5	Q9tpm5	agelaius ph
544	3	7.7	29	7	Q9XRK7	Q9xrk7	agelaius ph
545	3	7.7	29	7	Q9TPN6	Q9tpn6	agelaius ph
546	3	7.7	29	7	Q9TPM9	Q9tpm9	agelaius ph
547	3	7.7	29	7	Q9TPN5	Q9tpn5	agelaius ph
548	3	7.7	29	7	Q9TPM6	Q9tpm6	agelaius ph
549	3	7.7	29	7	Q9TPN2	Q9tpn2	agelaius ph
550	3	7.7	29	7	Q9XRK5	Q9xrk5	agelaius ph
551	3	7.7	29	7	Q9TPN1	Q9tpn1	agelaius ph
552	3	7.7	29	7	Q9XRD9	Q9xrd9	agelaius ph
553	3	7.7	29	7	Q30139	Q30139	homo sapien
554	3	7.7	29	7	Q9XRK3	Q9xrk3	agelaius ph
555	3	7.7	29	7	Q9TPN8	Q9tpn8	agelaius ph
556	3	7.7	29	7	Q9TPM7	Q9tpm7	agelaius ph
557	3	7.7	29	7	Q9TPP0	Q9tpp0	agelaius ph
558	3	7.7	29	7	Q9TPK6	Q9tpk6	agelaius ph
559	3	7.7	29	7	Q9TPN7	Q9tpn7	agelaius ph
560	3	7.7	29	7	Q9XRK4	Q9xrk4	agelaius ph
561	3	7.7	29	7	Q9TPM8	Q9tpm8	agelaius ph
562	3	7.7	29	7	Q9TPN4	Q9tpn4	agelaius ph
563	3	7.7	29	7	Q9TPN9	Q9tpn9	agelaius ph
564	3	7.7	29	7	Q06653	Q06653	homo sapien
565	3	7.7	29	8	Q9G5Z1	Q9g5z1	pseudocalot
566	3	7.7	29	8	Q9G657	Q9g657	japalura tr
567	3	7.7	29	8	Q9GF70	Q9gf70	trochodendr
568	3	7.7	29	8	Q9G615	Q9g615	cophotis ce
569	3	7.7	29	8	Q33131	Q33131	spinacia ol
570	3	7.7	29	8	Q9TI61	Q9ti61	allosyncarp

571	3	7.7	29	8	Q9G648	Q9g648 sitana pont
572	3	7.7	29	8	Q9G370	Q9g370 draco blanf
573	3	7.7	29	8	Q9G352	Q9g352 laudakia sa
574	3	7.7	29	8	O03087	O03087 anthoceros
575	3	7.7	29	8	Q8WD25	Q8wd25 ctenophorus
576	3	7.7	29	8	O03120	O03120 megaceros v
577	3	7.7	29	8	Q8HS21	Q8hs21 rheum x cul
578	3	7.7	29	9	Q9ZX23	Q9zx23 mycobacteri
579	3	7.7	29	10	Q9FUR9	Q9fur9 physcomitre
580	3	7.7	29	10	Q8RUM7	Q8rum7 zea mays (m
581	3	7.7	29	10	Q94JL6	Q94jl6 hevea brasi
582	3	7.7	29	10	Q42243	Q42243 arabidopsis
583	3	7.7	29	10	Q08065	Q08065 zea mays (m
584	3	7.7	29	10	Q8H772	Q8h772 arabidopsis
585	3	7.7	29	11	Q9CSI4	Q9csi4 mus musculu
586	3	7.7	29	11	Q9QVB1	Q9qvb1 rattus sp.
587	3	7.7	29	11	Q921Z6	Q921z6 mus musculu
588	3	7.7	29	11	Q64353	Q64353 mus musculu
589	3	7.7	29	11	O88214	O88214 mus musculu
590	3	7.7	29	11	Q8VIF4	Q8vif4 mus musculu
591	3	7.7	29	11	Q62777	Q62777 rattus norv
592	3	7.7	29	11	Q99JY5	Q99jy5 mus musculu
593	3	7.7	29	11	O88213	O88213 mus musculu
594	3	7.7	29	11	Q9QY65	Q9qy65 mus musculu
595	3	7.7	29	11	Q8R398	Q8r398 mus musculu
596	3	7.7	29	11	Q62300	Q62300 mus musculu
597	3	7.7	29	11	O08980	O08980 mus musculu
598	3	7.7	29	11	Q8CJ37	Q8cj37 mus musculu
599	3	7.7	29	12	Q91HB1	Q91hb1 porcine cir
600	3	7.7	29	12	O92646	O92646 hepatitis e
601	3	7.7	29	12	Q9DH48	Q9dh48 bovine coro
602	3	7.7	29	12	Q86872	Q86872 cauliflower
603	3	7.7	29	12	O92648	O92648 hepatitis e
604	3	7.7	29	12	O56835	O56835 vibrio chol
605	3	7.7	29	12	Q9QAR4	Q9qar4 bovine coro
606	3	7.7	29	13	O42547	O42547 brachydanio
607	3	7.7	29	13	P82234	P82234 rana tempor
608	3	7.7	29	13	Q8AYR0	Q8ayr0 oryzias lat
609	3	7.7	29	15	O72001	O72001 human endog
610	3	7.7	29	15	O71342	O71342 human endog
611	3	7.7	29	15	O71339	O71339 human endog
612	3	7.7	29	15	O71347	O71347 human endog
613	3	7.7	29	15	O71340	O71340 human endog
614	3	7.7	29	15	O71343	O71343 human endog
615	3	7.7	29	15	Q69897	Q69897 human immun
616	3	7.7	29	15	O71991	O71991 human endog
617	3	7.7	29	15	O71994	O71994 human endog
618	3	7.7	29	15	O71341	O71341 human endog
619	3	7.7	29	15	O71345	O71345 human endog
620	3	7.7	29	15	O71336	O71336 human endog
621	3	7.7	29	15	O71344	O71344 human endog
622	3	7.7	29	15	O71338	O71338 human endog
623	3	7.7	29	15	O71992	O71992 human endog
624	3	7.7	29	15	O71337	O71337 human endog
625	3	7.7	29	15	O71997	O71997 human endog
626	3	7.7	29	15	O71335	O71335 human endog
627	3	7.7	29	16	O25837	O25837 helicobacte

628	3	7.7	29	16	Q9KAV1	Q9kav1 bacillus ha
629	3	7.7	29	16	Q8ZP22	Q8zp22 salmonella
630	3	7.7	29	16	Q8ZL14	Q8zl14 salmonella
631	3	7.7	29	16	Q8X3T7	Q8x3t7 escherichia
632	3	7.7	29	16	Q8X3T6	Q8x3t6 escherichia
633	3	7.7	29	16	Q8X2E5	Q8x2e5 escherichia
634	3	7.7	29	16	Q8XU13	Q8xul3 ralstonia s
635	3	7.7	29	16	Q8PCQ6	Q8pcq6 xanthomonas
636	3	7.7	29	16	Q9X901	Q9x901 streptomyce
637	3	7.7	29	16	Q9S1T6	Q9slt6 streptomyce
638	3	7.7	29	16	Q8EQ82	Q8eq82 oceanobacil
639	3	7.7	29	16	Q8DFV6	Q8dfv6 vibrio vuln
640	3	7.7	29	17	Q8ZTM0	Q8ztm0 pyrobaculum
641	3	7.7	30	1	Q9UWK8	Q9uwk8 thermococcu
642	3	7.7	30	2	O85587	O85587 chlamydia t
643	3	7.7	30	2	Q9R8H1	Q9r8h1 chlamydia t
644	3	7.7	30	2	O85581	O85581 chlamydia t
645	3	7.7	30	2	Q9R8F6	Q9r8f6 chlamydia t
646	3	7.7	30	2	Q8KYE4	Q8kye4 bacillus an
647	3	7.7	30	2	Q9R5A3	Q9r5a3 pseudomonas
648	3	7.7	30	2	Q9R4K2	Q9r4k2 campylobact
649	3	7.7	30	2	Q9R8G2	Q9r8g2 chlamydia t
650	3	7.7	30	2	Q9R8I9	Q9r8i9 chlamydia t
651	3	7.7	30	2	Q9R8I3	Q9r8i3 chlamydia t
652	3	7.7	30	2	Q9RZY9	Q9rzy9 borrelia bu
653	3	7.7	30	2	Q9L8F9	Q9l8f9 klebsiella
654	3	7.7	30	2	O85563	O85563 chlamydia t
655	3	7.7	30	2	Q9R8G5	Q9r8g5 chlamydia t
656	3	7.7	30	2	Q9R8E5	Q9r8e5 chlamydia t
657	3	7.7	30	2	Q9R4J2	Q9r4j2 helicobacte
658	3	7.7	30	2	Q9R8H5	Q9r8h5 chlamydia t
659	3	7.7	30	2	Q44171	Q44171 anabaena sp
660	3	7.7	30	2	Q9R8I5	Q9r8i5 chlamydia t
661	3	7.7	30	2	Q9R8F8	Q9r8f8 chlamydia t
662	3	7.7	30	2	Q9R8F3	Q9r8f3 chlamydia t
663	3	7.7	30	2	Q47355	Q47355 escherichia
664	3	7.7	30	2	Q9R8F4	Q9r8f4 chlamydia t
665	3	7.7	30	2	Q9R8G7	Q9r8g7 chlamydia t
666	3	7.7	30	2	Q9R8I1	Q9r8i1 chlamydia t
667	3	7.7	30	2	Q9R8J1	Q9r8j1 chlamydia t
668	3	7.7	30	2	Q9R4A9	Q9r4a9 clostridium
669	3	7.7	30	2	Q9R8H9	Q9r8h9 chlamydia t
670	3	7.7	30	2	Q9K532	Q9k532 listeria mo
671	3	7.7	30	2	Q93GF6	Q93gf6 staphylococ
672	3	7.7	30	2	Q9R8H3	Q9r8h3 chlamydia t
673	3	7.7	30	2	Q9R8G0	Q9r8g0 chlamydia t
674	3	7.7	30	2	Q9R8G1	Q9r8g9 chlamydia t
675	3	7.7	30	2	Q9L8I9	Q9l8i9 enterobacte
676	3	7.7	30	2	Q9R530	Q9r530 escherichia
677	3	7.7	30	2	Q9R8H7	Q9r8h7 chlamydia t
678	3	7.7	30	2	Q9R5K3	Q9r5k3 leptospira
679	3	7.7	30	2	Q02800	Q02800 streptomyce
680	3	7.7	30	2	Q9R8I7	Q9r8i7 chlamydia t
681	3	7.7	30	2	Q9S014	Q9s014 borrelia bu
682	3	7.7	30	2	Q9R8F1	Q9r8f1 chlamydia t
683	3	7.7	30	2	Q9R4A8	Q9r4a8 clostridium
684	3	7.7	30	2	Q9RER6	Q9rer6 enterobacte

685	3	7.7	30	2	P83001	P83001	pseudomonas
686	3	7.7	30	2	P82134	P82134	corynebacte
687	3	7.7	30	2	Q8GQR2	Q8gqr2	bacillus my
688	3	7.7	30	2	Q8GQQ6	Q8gqq6	bacillus th
689	3	7.7	30	2	Q8GQQ4	Q8gqq4	bacillus th
690	3	7.7	30	2	Q8GF44	Q8gf44	zymomonas m
691	3	7.7	30	2	Q8G896	Q8g896	bacillus ce
692	3	7.7	30	2	Q8G895	Q8g895	bacillus ce
693	3	7.7	30	2	Q8G894	Q8g894	bacillus we
694	3	7.7	30	3	Q02213	Q02213	geotrichum
695	3	7.7	30	3	Q02176	Q02176	geotrichum
696	3	7.7	30	3	Q9URB6	Q9urb6	acremonium
697	3	7.7	30	4	Q16330	Q16330	homo sapien
698	3	7.7	30	4	Q96CZ0	Q96cz0	homo sapien
699	3	7.7	30	4	Q9UCW8	Q9ucw8	homo sapien
700	3	7.7	30	4	Q9UCW7	Q9ucw7	homo sapien
701	3	7.7	30	4	Q16113	Q16113	homo sapien
702	3	7.7	30	4	Q96D69	Q96d69	homo sapien
703	3	7.7	30	4	Q9UMJ2	Q9umj2	homo sapien
704	3	7.7	30	4	Q96Q60	Q96q60	homo sapien
705	3	7.7	30	4	Q14098	Q14098	homo sapien
706	3	7.7	30	4	Q99922	Q99922	homo sapien
707	3	7.7	30	4	Q9UBV5	Q9ubv5	homo sapien 50X,
708	3	7.7	30	4	Q9UC96	Q9uc96	homo sapien
709	3	7.7	30	4	Q96FR0	Q96fr0	homo sapien
710	3	7.7	30	4	Q8WUP3	Q8wup3	homo sapien
711	3	7.7	30	4	Q9BWZ3	Q9bwz3	homo sapien
712	3	7.7	30	4	P78542	P78542	homo sapien
713	3	7.7	30	5	Q27545	Q27545	crithidia f
714	3	7.7	30	5	Q8WSM0	Q8wsm0	caenorhabdi
715	3	7.7	30	5	Q95PT1	Q95pt1	leishmania
716	3	7.7	30	5	Q9BM72	Q9bm72	drosophila
717	3	7.7	30	5	Q8I868	Q8i868	acanthamoeb
718	3	7.7	30	6	Q28321	Q28321	capra hircu
719	3	7.7	30	6	Q9TS67	Q9ts67	sus
720	3	7.7	30	6	Q95M52	Q95m52	bos taurus
721	3	7.7	30	6	Q28323	Q28323	capra hircu
722	3	7.7	30	6	Q9MZX0	Q9mzx0	colobus pol
723	3	7.7	30	6	Q8SPU1	Q8spu1	macaca mula
724	3	7.7	30	6	Q9TQQ6	Q9tqq6	canis famil
725	3	7.7	30	6	Q9TTF9	Q9ttf9	ateles belz
726	3	7.7	30	6	O46424	O46424	oryctolagus
727	3	7.7	30	8	Q9T2V9	Q9t2v9	cochliobolu
728	3	7.7	30	8	Q9MJF6	Q9mjf6	candida alb
729	3	7.7	30	8	Q8M0A1	Q8m0a1	bucorvus le
730	3	7.7	30	8	Q94TX1	Q94tx1	lithodes ma
731	3	7.7	30	8	Q9T2P9	Q9t2p9	narcissus p
732	3	7.7	30	8	Q34897	Q34897	lasiorhinus
733	3	7.7	30	8	Q8M2G1	Q8m2g1	vestiaria c
734	3	7.7	30	8	Q9T2P2	Q9t2p2	rattus sp.
735	3	7.7	30	8	Q95F79	Q95f79	hizikia fus
736	3	7.7	30	8	Q9TI56	Q9ti56	eucalyptus
737	3	7.7	30	9	Q8W674	Q8w674	enterobacte
738	3	7.7	30	10	Q9FQX4	Q9fqx4	oncidium cv
739	3	7.7	30	10	O23933	O23933	flaveria tr
740	3	7.7	30	10	Q93WY2	Q93wy2	oryza sativ
741	3	7.7	30	10	Q9FRA1	Q9fra1	oryza sativ

742	3	7.7	30	10	Q41490	Q41490	solanum tub
743	3	7.7	30	11	Q8K3D0	Q8k3d0	mus musculu
744	3	7.7	30	11	Q9QVC3	Q9qvc3	rattus sp.
745	3	7.7	30	11	Q9QV39	Q9qv39	rattus sp.
746	3	7.7	30	11	Q9QV43	Q9qv43	rattus sp.
747	3	7.7	30	11	Q8R4W3	Q8r4w3	mus musculu
748	3	7.7	30	11	Q8K4T8	Q8k4t8	rattus norv
749	3	7.7	30	11	Q8R4W4	Q8r4w4	mus musculu
750	3	7.7	30	11	Q9QV44	Q9qv44	mus sp. and
751	3	7.7	30	11	Q9JHC2	Q9jhc2	rattus norv
752	3	7.7	30	11	Q8K4T7	Q8k4t7	rattus norv
753	3	7.7	30	11	Q9WUS6	Q9wus6	mus musculu
754	3	7.7	30	11	Q9QV06	Q9qv06	rattus sp.
755	3	7.7	30	11	Q8BR32	Q8br32	mus musculu
756	3	7.7	30	12	Q9QS22	Q9qs22	hepatitis b
757	3	7.7	30	12	Q9QS36	Q9qs36	hepatitis b
758	3	7.7	30	12	Q9QS20	Q9qs20	hepatitis b
759	3	7.7	30	12	Q9QS16	Q9qs16	hepatitis b
760	3	7.7	30	12	Q9QS28	Q9qs28	hepatitis b
761	3	7.7	30	12	Q9QS53	Q9qs53	hepatitis b
762	3	7.7	30	12	Q9QS24	Q9qs24	hepatitis b
763	3	7.7	30	12	Q9QS43	Q9qs43	hepatitis b
764	3	7.7	30	12	Q9QS39	Q9qs39	hepatitis b
765	3	7.7	30	12	Q9QS13	Q9qs13	hepatitis b
766	3	7.7	30	12	Q9QS45	Q9qs45	hepatitis b
767	3	7.7	30	12	Q9QS47	Q9qs47	hepatitis b
768	3	7.7	30	12	Q9QS40	Q9qs40	hepatitis b
769	3	7.7	30	12	Q9QS14	Q9qs14	hepatitis b
770	3	7.7	30	12	Q9QS52	Q9qs52	hepatitis b
771	3	7.7	30	12	Q9QS33	Q9qs33	hepatitis b
772	3	7.7	30	12	Q9QS19	Q9qs19	hepatitis b
773	3	7.7	30	12	Q9QS51	Q9qs51	hepatitis b
774	3	7.7	30	12	Q91HB8	Q91hb8	tt virus. o
775	3	7.7	30	12	Q9QS29	Q9qs29	hepatitis b
776	3	7.7	30	12	Q9QS49	Q9qs49	hepatitis b
777	3	7.7	30	12	Q9QS50	Q9qs50	hepatitis b
778	3	7.7	30	12	Q9QS12	Q9qs12	hepatitis b
779	3	7.7	30	12	Q9QS37	Q9qs37	hepatitis b
780	3	7.7	30	12	Q9QS17	Q9qs17	hepatitis b
781	3	7.7	30	12	Q9QS32	Q9qs32	hepatitis b
782	3	7.7	30	12	Q9IJV5	Q9ijv5	norwalk vir
783	3	7.7	30	12	Q9QS48	Q9qs48	hepatitis b
784	3	7.7	30	12	Q9QS21	Q9qs21	hepatitis b
785	3	7.7	30	12	Q9QS27	Q9qs27	hepatitis b
786	3	7.7	30	12	Q9QS41	Q9qs41	hepatitis b
787	3	7.7	30	12	Q9QS15	Q9qs15	hepatitis b
788	3	7.7	30	12	Q9QS38	Q9qs38	hepatitis b
789	3	7.7	30	12	Q9QS30	Q9qs30	hepatitis b
790	3	7.7	30	12	Q86870	Q86870	cauliflower
791	3	7.7	30	12	Q9QS31	Q9qs31	hepatitis b
792	3	7.7	30	12	Q9QS11	Q9qs11	hepatitis b
793	3	7.7	30	12	Q9QS26	Q9qs26	hepatitis b
794	3	7.7	30	12	Q9QS46	Q9qs46	hepatitis b
795	3	7.7	30	12	Q66858	Q66858	foot-and-mo
796	3	7.7	30	12	Q9QS18	Q9qs18	hepatitis b
797	3	7.7	30	12	Q9QS44	Q9qs44	hepatitis b
798	3	7.7	30	12	Q9QS25	Q9qs25	hepatitis b

799	3	7.7	30	12	Q9QS34	Q9qs34	hepatitis b
800	3	7.7	30	12	Q9QS42	Q9qs42	hepatitis b
801	3	7.7	30	12	Q9WLK3	Q9wlk3	hepatitis e
802	3	7.7	30	12	Q66859	Q66859	foot-and-mo
803	3	7.7	30	12	Q96630	Q96630	bovine aden
804	3	7.7	30	12	Q9QS23	Q9qs23	hepatitis b
805	3	7.7	30	12	Q9QS35	Q9qs35	hepatitis b
806	3	7.7	30	13	Q9PRX3	Q9prx3	xenopus lae
807	3	7.7	30	13	Q9YGG6	Q9ygg6	xiphophorus
808	3	7.7	30	13	Q9YGG5	Q9ygg5	xiphophorus
809	3	7.7	30	13	Q9YGG2	Q9ygg2	xiphophorus
810	3	7.7	30	13	Q9YGF9	Q9ygf9	xiphophorus
811	3	7.7	30	13	Q9YGG7	Q9ygg7	xiphophorus
812	3	7.7	30	13	Q9YGG4	Q9ygg4	xiphophorus
813	3	7.7	30	13	Q9YGG3	Q9ygg3	xiphophorus
814	3	7.7	30	13	Q9YGD5	Q9ygd5	xiphophorus
815	3	7.7	30	15	P90307	P90307	human immun
816	3	7.7	30	15	Q86599	Q86599	human endog
817	3	7.7	30	15	Q9WJA9	Q9wja9	human immun
818	3	7.7	30	15	Q991P5	Q991p5	human immun
819	3	7.7	30	15	Q03514	Q03514	mouse intra
820	3	7.7	30	16	O24869	O24869	helicobacte
821	3	7.7	30	16	O50822	O50822	borrelia bu
822	3	7.7	30	16	O50910	O50910	borrelia bu
823	3	7.7	30	16	Q9X0W9	Q9x0w9	thermotoga
824	3	7.7	30	16	Q9X066	Q9x066	thermotoga
825	3	7.7	30	16	Q9WZ86	Q9wz86	thermotoga
826	3	7.7	30	16	Q9PA01	Q9pa01	xylella fas
827	3	7.7	30	16	Q9KV65	Q9kv65	vibrio chol
828	3	7.7	30	16	Q9KQQ5	Q9kqq5	vibrio chol
829	3	7.7	30	16	Q9KPR0	Q9kpr0	vibrio chol
830	3	7.7	30	16	Q9KNF2	Q9knf2	vibrio chol
831	3	7.7	30	16	Q9KLP5	Q9klp5	vibrio chol
832	3	7.7	30	16	Q9K7Y1	Q9k7y1	bacillus ha
833	3	7.7	30	16	Q9JUP4	Q9jup4	neisseria m
834	3	7.7	30	16	Q9I5K7	Q9i5k7	pseudomonas
835	3	7.7	30	16	Q98NK7	Q98nk7	rhizobium l
836	3	7.7	30	16	Q98LE7	Q98le7	rhizobium l
837	3	7.7	30	16	Q97SR7	Q97sr7	streptococc
838	3	7.7	30	16	Q97R13	Q97r13	streptococc
839	3	7.7	30	16	Q8X4J3	Q8x4j3	escherichia
840	3	7.7	30	16	Q99VB7	Q99vb7	staphylococ
841	3	7.7	30	16	Q8G1R1	Q8glr1	brucella su
842	3	7.7	30	16	Q8G036	Q8g036	brucella su
843	3	7.7	30	16	Q8FZX9	Q8fzx9	brucella su
844	3	7.7	30	16	Q8FXU3	Q8fxu3	brucella su
845	3	7.7	30	16	Q8EKP1	Q8ekp1	shewanella
846	3	7.7	30	16	Q8EJS7	Q8ejs7	shewanella
847	3	7.7	30	16	Q8EJP3	Q8ejp3	shewanella
848	3	7.7	30	16	Q8EHK5	Q8ehk5	shewanella
849	3	7.7	30	16	Q8EG27	Q8eg27	shewanella
850	3	7.7	30	16	Q8EFH6	Q8efh6	shewanella
851	3	7.7	30	16	Q8ECK7	Q8eck7	shewanella
852	3	7.7	30	16	Q8EB32	Q8eb32	shewanella
853	3	7.7	30	16	Q8EAV6	Q8eav6	shewanella
854	3	7.7	30	16	Q8DZ13	Q8dz13	streptococc
855	3	7.7	30	16	Q8DS00	Q8ds00	streptococc

856	3	7.7	30	16	Q8CU88	Q8cu88 staphylococ
857	3	7.7	30	16	Q8CRR1	Q8crr1 staphylococ
858	3	7.7	30	16	Q8CKB0	Q8ckb0 yersinia pe
859	3	7.7	30	17	Q9HMB0	Q9hmb0 halobacteri
860	3	7.7	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
861	3	7.7	31	1	Q8X254	Q8x254 halobacteri
862	3	7.7	31	2	Q54825	Q54825 streptococc
863	3	7.7	31	2	Q53449	Q53449 chlamydia t
864	3	7.7	31	2	Q9K4X1	Q9k4x1 planktothri
865	3	7.7	31	2	Q9S619	Q9s619 prochloroco
866	3	7.7	31	2	Q9L7N5	Q9l7n5 borrelia bi
867	3	7.7	31	2	Q9S0E6	Q9s0e6 borrelia bu
868	3	7.7	31	2	Q9X3C3	Q9x3c3 prochloroco
869	3	7.7	31	2	Q47374	Q47374 escherichia
870	3	7.7	31	2	Q9R2N7	Q9r2n7 escherichia
871	3	7.7	31	2	Q9K4X9	Q9k4x9 planktothri
872	3	7.7	31	2	Q9F1I5	Q9f1i5 enterococcu
873	3	7.7	31	2	Q8KYP8	Q8kyp8 bacillus an
874	3	7.7	31	2	Q9R503	Q9r503 thermotoga
875	3	7.7	31	2	Q9L7N3	Q9l7n3 borrelia an
876	3	7.7	31	2	Q47353	Q47353 escherichia
877	3	7.7	31	2	Q9RHP1	Q9rhp1 escherichia
878	3	7.7	31	2	Q8RTS5	Q8rts5 uncultured
879	3	7.7	31	2	Q9R2G0	Q9r2g0 staphylococ
880	3	7.7	31	2	Q52917	Q52917 rhizobium m
881	3	7.7	31	2	Q53411	Q53411 bacillus su
882	3	7.7	31	2	O32325	O32325 clostridium
883	3	7.7	31	2	Q8L3M4	Q8l3m4 rickettsia
884	3	7.7	31	2	O69420	O69420 escherichia
885	3	7.7	31	2	Q9EV62	Q9ev62 streptococc
886	3	7.7	31	2	Q47364	Q47364 escherichia
887	3	7.7	31	2	Q44263	Q44263 aeromonas s
888	3	7.7	31	2	Q49248	Q49248 mycoplasma
889	3	7.7	31	3	O94120	O94120 saccharomyc
890	3	7.7	31	4	Q9UMG3	Q9umg3 o sapien
891	3	7.7	31	4	Q9BQU1	Q9bqu1 homo sapien
892	3	7.7	31	4	Q8N6N1	Q8n6n1 homo sapien
893	3	7.7	31	4	Q9UCF2	Q9ucf2 homo sapien
894	3	7.7	31	4	Q9UJ40	Q9uj40 homo sapien
895	3	7.7	31	4	Q9UEI3	Q9uei3 homo sapien
896	3	7.7	31	4	Q9Y2A3	Q9y2a3 homo sapien
897	3	7.7	31	4	Q8NEI8	Q8nei8 homo sapien
898	3	7.7	31	4	Q9UDK2	Q9udk2 homo sapien
899	3	7.7	31	4	Q8WYF5	Q8wyf5 homo sapien
900	3	7.7	31	4	Q96FE4	Q96fe4 homo sapien
901	3	7.7	31	4	Q8WYF3	Q8wyf3 homo sapien
902	3	7.7	31	4	Q8N5X3	
903	3	7.7	31	4	Q99893	Q99893 homo sapien
904	3	7.7	31	4	Q9UBW3	Q9ubw3 homo sapien
905	3	7.7	31	4	Q96Q71	Q96q71 homo sapien
906	3	7.7	31	4	Q8TBX1	Q8tbx1 homo sapien
907	3	7.7	31	5	Q19924	Q19924 caenorhabdi
908	3	7.7	31	5	Q26760	Q26760 trypanosoma
909	3	7.7	31	5	Q26761	Q26761 trypanosoma
910	3	7.7	31	5	Q26762	Q26762 trypanosoma
911	3	7.7	31	5	Q8STH5	Q8sth5 drosophila
912	3	7.7	31	5	Q9NGN5	Q9ngn5 strongyloce

913	3	7.7	31	5	Q17165	Q17165	brugia mala
914	3	7.7	31	5	Q8IF28	Q8if28	trypanosoma
915	3	7.7	31	5	Q8IEY3	Q8iey3	trypanosoma
916	3	7.7	31	6	Q9TRJ3	Q9trj3	canis famil
917	3	7.7	31	6	Q28325	Q28325	capra hircu
918	3	7.7	31	6	Q9TR79	Q9tr79	ovis aries
919	3	7.7	31	6	Q9GLD6	Q9gld6	sus scrofa
920	3	7.7	31	6	Q9BEI0	Q9bei0	monodelphis
921	3	7.7	31	6	Q9BDF3	Q9bdf3	orycteropus
922	3	7.7	31	6	Q9XS80	Q9xs80	sus scrofa
923	3	7.7	31	6	Q9TR61	Q9tr61	canis famil
924	3	7.7	31	6	Q9TSE4	Q9tse4	oryctolagus
925	3	7.7	31	6	Q9GJZ3	Q9gjz3	dugong dugo
926	3	7.7	31	7	Q29868	Q29868	homo sapien
927	3	7.7	31	7	Q9MWI7	Q9mwi7	geospiza sc
928	3	7.7	31	8	Q9T690	Q9t690	gecko gecko
929	3	7.7	31	8	Q8MBD7	Q8mbd7	astripomoea
930	3	7.7	31	8	Q9MNM2	Q9mmm2	bufo americ
931	3	7.7	31	8	Q36709	Q36709	ophiopholis
932	3	7.7	31	8	Q94NH2	Q94nh2	littorina s
933	3	7.7	31	8	Q9MS68	Q9ms68	euglena des
934	3	7.7	31	8	Q33577	Q33577	trypanosoma
935	3	7.7	31	8	Q9TKW5	Q9tkw5	nephroselmi
936	3	7.7	31	8	Q8MB91	Q8mb91	convolvulus
937	3	7.7	31	9	Q9B083	Q9b083	mycobacteri
938	3	7.7	31	9	O64265	O64265	mycobacteri
939	3	7.7	31	10	Q9SPF4	Q9spf4	vitis vinif
940	3	7.7	31	10	Q9M3S3	Q9m3s3	arabidopsis
941	3	7.7	31	10	Q8IMG1	Q8img1	oryza sativ
942	3	7.7	31	10	Q9SPF5	Q9spf5	vitis vinif
943	3	7.7	31	11	Q9QVA5	Q9qva5	cavia (guin
944	3	7.7	31	11	Q9QXB6	Q9qxb6	mus musculu
945	3	7.7	31	11	Q9ESY0	Q9esy0	mus musculu
946	3	7.7	31	11	Q99KK6	Q99kk6	mus musculu
947	3	7.7	31	11	Q9WUS8	Q9wus8	mus musculu
948	3	7.7	31	11	Q99PC8	Q99pc8	rattus norv
949	3	7.7	31	11	Q922Z6	Q922z6	mus musculu
950	3	7.7	31	11	Q9QYY4	Q9qyy4	mus musculu
951	3	7.7	31	11	Q8CGM7	Q8cgm7	mus musculu
952	3	7.7	31	12	Q8JSB4	Q8jsb4	hepatitis b
953	3	7.7	31	12	Q68024	Q68024	hepatitis b
954	3	7.7	31	12	Q8JS95	Q8js95	hepatitis b
955	3	7.7	31	12	Q67979	Q67979	hepatitis b
956	3	7.7	31	12	Q8JSB3	Q8jsb3	hepatitis b
957	3	7.7	31	12	Q68058	Q68058	hepatitis b
958	3	7.7	31	12	Q8JS78	Q8js78	hepatitis b
959	3	7.7	31	12	Q8JS97	Q8js97	hepatitis b
960	3	7.7	31	12	Q68049	Q68049	hepatitis b
961	3	7.7	31	12	Q67967	Q67967	hepatitis b
962	3	7.7	31	12	Q8JS90	Q8js90	hepatitis b
963	3	7.7	31	12	Q8JSB0	Q8jsb0	hepatitis b
964	3	7.7	31	12	Q8JSC6	Q8jsc6	hepatitis b
965	3	7.7	31	12	Q67987	Q67987	hepatitis b
966	3	7.7	31	12	Q8JSB7	Q8jsb7	hepatitis b
967	3	7.7	31	12	Q8JS83	Q8js83	hepatitis b
968	3	7.7	31	12	Q67992	Q67992	hepatitis b
969	3	7.7	31	12	Q68080	Q68080	hepatitis b

970	3	7.7	31	12	Q68002	Q68002 hepatitis b
971	3	7.7	31	12	Q68013	Q68013 hepatitis b
972	3	7.7	31	12	Q8JS98	Q8js98 hepatitis b
973	3	7.7	31	12	Q68050	Q68050 hepatitis b
974	3	7.7	31	12	Q8JSB6	Q8jsb6 hepatitis b
975	3	7.7	31	12	Q68004	Q68004 hepatitis b
976	3	7.7	31	12	Q8JS93	Q8js93 hepatitis b
977	3	7.7	31	12	Q8JSA4	Q8jsa4 hepatitis b
978	3	7.7	31	12	Q8JS84	Q8js84 hepatitis b
979	3	7.7	31	12	Q68019	Q68019 hepatitis b
980	3	7.7	31	12	073430	073430 human papil
981	3	7.7	31	12	Q9PXL2	Q9pxl2 hepatitis b
982	3	7.7	31	12	Q8JSA0	Q8jsa0 hepatitis b
983	3	7.7	31	12	Q8JSD5	Q8jsd5 hepatitis b
984	3	7.7	31	12	Q67998	Q67998 hepatitis b
985	3	7.7	31	12	Q68056	Q68056 hepatitis b
986	3	7.7	31	12	Q68033	Q68033 hepatitis b
987	3	7.7	31	12	Q68018	Q68018 hepatitis b
988	3	7.7	31	12	Q68011	Q68011 hepatitis b
989	3	7.7	31	12	Q8JS74	Q8js74 hepatitis b
990	3	7.7	31	12	Q8JS66	Q8js66 hepatitis b
991	3	7.7	31	12	Q68071	Q68071 hepatitis b
992	3	7.7	31	12	Q8JS81	Q8js81 hepatitis b
993	3	7.7	31	12	Q67957	Q67957 hepatitis b
994	3	7.7	31	12	Q67983	Q67983 hepatitis b
995	3	7.7	31	12	Q67985	Q67985 hepatitis b
996	3	7.7	31	12	Q67962	Q67962 hepatitis b
997	3	7.7	31	12	Q67990	Q67990 hepatitis b
998	3	7.7	31	12	Q68034	Q68034 hepatitis b
999	3	7.7	31	12	Q68046	Q68046 hepatitis b
1000	3	7.7	31	12	Q68000	Q68000 hepatitis b

ALIGNMENTS

RESULT 1

Q8P6H8

ID Q8P6H8 PRELIMINARY; PRT; 37 AA.

AC Q8P6H8;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Phage-related protein.

GN ORF52 OR XCC2991.

OS *Xanthomonas campestris* (pv. *campestris*).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorrry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012413; AAM42263.1; -.
KW Complete proteome.
SQ SEQUENCE 37 AA; 4295 MW; 41E2614125B1A922 CRC64;

Query Match 15.4%; Score 6; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARL 16
|||||
Db 27 RERARL 32

RESULT 2

Q8FVK2

ID Q8FVK2 PRELIMINARY; PRT; 38 AA.
AC Q8FVK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN BRA0835.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014577; AAN34010.1; -.
DR TIGR; BRA0835; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 38 AA; 4255 MW; D71AA8D253FD7F86 CRC64;

Query Match 15.4%; Score 6; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERARLL 17
|||||
Db 6 ERARLL 11

RESULT 3

Q9TWE2

ID Q9TWE2 PRELIMINARY; PRT; 28 AA.
AC Q9TWE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE AXONEMAL alpha-tubulin isoform (Fragment).
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE.
RX MEDLINE=96215272; PubMed=8626629;
RA Mary J., Redeker V., Le Caer J.P., Rossier J., Schmitter J.M.;
RT "Posttranslational modifications in the C-terminal tail of axonemal
RT tubulin from sea urchin sperm.";
RL J. Biol. Chem. 271:9928-9933(1996).
SQ SEQUENCE 28 AA; 3104 MW; 9C50E220D1AFD7C1 CRC64;

Query Match 12.8%; Score 5; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALe 21
|||||
Db 2 LAALe 6

RESULT 4

Q9WTS1

ID Q9WTS1 PRELIMINARY; PRT; 28 AA.
AC Q9WTS1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Egfr (Fragment).
GN EGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondoh S.K., Akiyama N.;

RT "Rat EGFR promoter from NRK cells.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB025197; BAA76391.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2855 MW; B56EAB41A074D15A CRC64;

Query Match 12.8%; Score 5; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 14 LLAAL 18

RESULT 5

Q9TTP2

ID Q9TTP2 PRELIMINARY; PRT; 29 AA.
AC Q9TTP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
GN AGT.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20188798; PubMed=10723739;
RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
RT in primates.";
RL Mol. Biol. Evol. 17:387-400(2000).
DR EMBL; AJ237886; CAB56803.1; -.
KW Aminotransferase; Transferase.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3048 MW; 51645B5E27835DC3 CRC64;

Query Match 12.8%; Score 5; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 HKLLV 35
|||
Db 4 HKLLV 8

RESULT 6

Q9JLR6

ID Q9JLR6 PRELIMINARY; PRT; 29 AA.
AC Q9JLR6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Epidermal growth factor receptor (Fragment).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RX MEDLINE=20167208; PubMed=10702298;
 RA Liu X.-W., Katagiri Y., Jiang H., Gong L.-J., Guo L.-Y., Shibutani M.,
 RA Johnson A.C., Guroff G.;
 RT "Cloning and Characterization of the Promoter Region of the Rat
 RT Epidermal Growth Factor Receptor Gene and Its Transcriptional
 RT Regulation by Nerve Growth Factor in PC12 Cells.";
 RL J. Biol. Chem. 275:7280-7288(2000).
 DR EMBL; AF142153; AAF27540.1; -.
 KW Receptor.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2984 MW; 1A056EAB41A074D1 CRC64;

Query Match 12.8%; Score 5; DB 11; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 14 LLAAL 18

RESULT 7

Q9I390

ID Q9I390 PRELIMINARY; PRT; 29 AA.
 AC Q9I390;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE KdpF protein.
 GN KDPF OR PA1632.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004591; AAG05021.1; -.
 KW Complete proteome.
 SQ SEQUENCE 29 AA; 3206 MW; 031E034AF96C0392 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||||
Db 8 SLALA 12

RESULT 8

Q9RHF9

ID Q9RHF9 PRELIMINARY; PRT; 31 AA.
AC Q9RHF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Acinetobacter calcoaceticus.
OG Plasmid pKLH1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=aberrant mercury resistance transposon;
RA Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
RA Yurieva O.V., Nikiforov V.G.;
RT "pKLH1-like aberrant mercury resistance transposons of environmental
RT Acinetobacter strains: spread, polymorphism and possible origin."
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ251517; CAB65941.1; -.
DR InterPro; IPR001802; HG_scavenger.
DR PRINTS; PR00946; HGSCAVENGER.
KW Plasmid.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3182 MW; 2EBCF50B7D9BC66E CRC64;

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||||
Db 7 SLALA 11

RESULT 9

Q9T1K0

ID Q9T1K0 PRELIMINARY; PRT; 31 AA.
AC Q9T1K0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).

GN STX2.
 OS Bacteriophage F6.
 OC Viruses.
 OX NCBI_TaxID=108918;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F6;
 RX MEDLINE=98320580; PubMed=9647813;
 RA Muniesa M., Jofre J.;
 RT "Abundance in sewage of bacteriophages that infect Escherichia coli
 RT O157:H7 and that carry the Shiga toxin 2 gene.";
 RL Appl. Environ. Microbiol. 64:2443-2448(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F6;
 RX MEDLINE=20117821; PubMed=10650226;
 RA Muniesa M., Jofre J.;
 RT "Occurrence of phages infecting Escherichia coli O157:H7 carrying the
 RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251234; CAB61566.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
 |||||
 Db 14 AALER 18

RESULT 10

Q9T1K2

ID Q9T1K2 PRELIMINARY; PRT; 31 AA.
 AC Q9T1K2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
 DE (Fragment).
 GN STX2.
 OS Bacteriophage F3.
 OC Viruses.
 OX NCBI_TaxID=108916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F3;
 RX MEDLINE=98320580; PubMed=9647813;
 RA Muniesa M., Jofre J.;

RT "Abundance in sewage of bacteriophages that infect Escherichia coli
 RT 0157:H7 and that carry the Shiga toxin 2 gene.";
 RL Appl. Environ. Microbiol. 64:2443-2448(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F3;
 RX MEDLINE=20117821; PubMed=10650226;
 RA Muniesa M., Jofre J.;
 RT "Occurrence of phages infecting Escherichia coli 0157:H7 carrying the
 RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251232; CAB61564.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AALER 22
 |||||
 Db 14 AALER 18

RESULT 11

Q9T1K1

ID Q9T1K1 PRELIMINARY; PRT; 31 AA.
 AC Q9T1K1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
 DE (Fragment).
 GN STX2.
 OS Bacteriophage F5.
 OC Viruses.
 OX NCBI_TaxID=108917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F5;
 RX MEDLINE=98320580; PubMed=9647813;
 RA Muniesa M., Jofre J.;
 RT "Abundance in sewage of bacteriophages that infect Escherichia coli
 RT 0157:H7 and that carry the Shiga toxin 2 gene.";
 RL Appl. Environ. Microbiol. 64:2443-2448(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F5;
 RX MEDLINE=20117821; PubMed=10650226;
 RA Muniesa M., Jofre J.;
 RT "Occurrence of phages infecting Escherichia coli 0157:H7 carrying the

RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251233; CAB61565.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
 |||||
 Db 14 AALER 18

RESULT 12

Q9T1K3

ID Q9T1K3 PRELIMINARY; PRT; 31 AA.
 AC Q9T1K3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
 DE (Fragment).
 GN STX2.
 OS Bacteriophage f1.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=10863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;
 RX MEDLINE=98320580; PubMed=9647813;
 RA Muniesa M., Jofre J.;
 RT "Abundance in sewage of bacteriophages that infect Escherichia coli
 RT O157:H7 and that carry the Shiga toxin 2 gene.";
 RL Appl. Environ. Microbiol. 64:2443-2448(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;
 RX MEDLINE=20117821; PubMed=10650226;
 RA Muniesa M., Jofre J.;
 RT "Occurrence of phages infecting Escherichia coli O157:H7 carrying the
 RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251231; CAB61563.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.

FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
|||||
Db 14 AALER 18

RESULT 13

Q9KM83

ID Q9KM83 PRELIMINARY; PRT; 33 AA.
AC Q9KM83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein VCA0500.
GN VCA0500.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004381; AAF96403.1; -.
DR TIGR; VCA0500; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 3731 MW; 625DB1FF2E10E8A0 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAAF 10
|||||
Db 16 DDAAF 20

RESULT 14

Q8XY48

ID Q8XY48 PRELIMINARY; PRT; 33 AA.
AC Q8XY48;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Probable phage-related protein fragment.
 GN RSC1915 OR RS03485.
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646067; CAD15617.1; -.
 KW Complete proteome.
 SQ SEQUENCE 33 AA; 4036 MW; 41DF9B7705EC474D CRC64;

Query Match 12.8%; Score 5; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERAR 15
 |||||
 Db 22 RERAR 26

RESULT 15

Q27372

ID Q27372 PRELIMINARY; PRT; 37 AA.
 AC Q27372;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE (Clone 11) U1 snRNA, 3' end of CDS (Fragment).
 GN U1 SNRNA.
 OS *Bombyx mori* (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111299; PubMed=8589846;
 RA Gao J.P., Herrera R.J.;
 RT "U1 snRNA variants coexist in *Bombyx mori* cells.";
 RL Insect Mol. Biol. 4:193-202(1995).
 DR EMBL; L42957; AAB00485.1; -.
 DR EMBL; L42955; AAB00483.1; -.
 FT NON_TER 1 1

SQ SEQUENCE 37 AA; 4187 MW; 2541733F7C9D68FA CRC64;

Query Match 12.8%; Score 5; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLL 17
|||||
Db 10 RARLL 14

RESULT 16

Q8SYH5

ID Q8SYH5 PRELIMINARY; PRT; 37 AA.
AC Q8SYH5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE RE58095p.
GN BCDNA:RE58095.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY071546; AAL49168.1; -.
DR FlyBase; FBgn0047081; BcDNA:RE58095.
SQ SEQUENCE 37 AA; 4505 MW; 98148EB2DD00287C CRC64;

Query Match 12.8%; Score 5; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERAR 15
|||||
Db 20 RERAR 24

RESULT 17

Q9TTR4

ID Q9TTR4 PRELIMINARY; PRT; 37 AA.
AC Q9TTR4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
GN AGT.

OS Cercopithecus diana (Diana monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=36224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=);
 RX MEDLINE=20188798; PubMed=10723739;
 RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
 RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
 RT in primates.";
 RL Mol. Biol. Evol. 17:387-400(2000).
 DR EMBL; AJ237891; CAB56774.1; -.
 KW Aminotransferase; Transferase.
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 3979 MW; 7289022410A60DF1 CRC64;

Query Match 12.8%; Score 5; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 HKLLV 35
 |||||
 Db 4 HKLLV 8

RESULT 18

Q9N260

ID Q9N260 PRELIMINARY; PRT; 37 AA.
 AC Q9N260;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MADH4 protein (Fragment).
 GN MADH4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20118593; PubMed=10654432;
 RA Kelly K.A., Larsen N.J., Marklund S., Rothschild M.F.;
 RT "Mapping of two tumor suppressor genes in the pig.";
 RL Anim. Biotechnol. 10:81-85(1999).
 DR EMBL; AF120280; AAF70206.1; -.
 DR HSSP; Q13485; 1YGS.
 DR InterPro; IPR001132; Dwarfin.
 DR Pfam; PF03166; MH2; 1.
 FT NON_TER 1 1
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 4038 MW; EDFA3087D75E7B30 CRC64;

Query Match 12.8%; Score 5; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERARL 16
 |||||
 Db 26 ERARL 30

RESULT 19

Q9H4Y8

ID Q9H4Y8 PRELIMINARY; PRT; 38 AA.
 AC Q9H4Y8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE DJ1041C10.1 (Beta-1,4-galactosyltransferase, polypeptide 5) (Beta-1.4-
 DE galactosyltransferase V) (Fragment).
 GN B4GALT5 OR GT-V.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Heath P.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Sato T.;
 RT "Promoter analysis of human beta-1,4-galactosyltransferase V gene."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL162615; CAC11145.1; -.
 DR EMBL; AB067772; BAC07182.1; -.
 KW Glycosyltransferase; Transferase.
 FT NON_TER 38 38
 SQ SEQUENCE 38 AA; 4359 MW; ECC7FA6515263101 CRC64;

Query Match 12.8%; Score 5; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 15 LLAAL 19

RESULT 20

Q8U580

ID Q8U580 PRELIMINARY; PRT; 38 AA.
 AC Q8U580;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE AGR_C_3308p.
 GN AGR_C_3308.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL; AE008101; AAK87568.1; -.
 SQ SEQUENCE 38 AA; 4583 MW; 9D7E1BD01CDC0F78 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
 |||||
 Db 16 KLLVL 20

RESULT 21

Q9LB47

ID Q9LB47 PRELIMINARY; PRT; 39 AA.
 AC Q9LB47;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Vacuolating cytotoxin (Fragment).
 GN VACA.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G21;
 RA Ji X., Telford J.L., Burroni D., Guidotti S., Pagliaccia C.,
 RA Rayrat J.M., Xu G., Rappuoli R.;
 RT "Allelic variation of vacA gene in the Chinese Helicobacter pylori.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF050405; AAF26587.1; -.
 DR InterPro; IPR003842; VacA.
 DR PRINTS; PR01656; VACCYTOTOXIN.
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4308 MW; 18CA80FCE9D4C92C CRC64;

Query Match 12.8%; Score 5; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
 |||||

Db 16 SLALA 20

RESULT 22

Q9UDI2

ID Q9UDI2 PRELIMINARY; PRT; 39 AA.
AC Q9UDI2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Neutrophil cytosolic factor 3; NCF-3 (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93277853; PubMed=8504089;
RA Kwong C.H., Malech H.L., Rotrosen D., Leto T.L.;
RT "Regulation of the human neutrophil NADPH oxidase by rho-related G-
RT proteins.";
RL Biochemistry 32:5711-5717(1993).
DR HSSP; P25763; 1A4R.
FT NON_TER 1 1
FT NON_CONS 11 12
FT NON_CONS 22 23
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4405 MW; 591520724F66E350 CRC64;

Query Match 12.8%; Score 5; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
|||
Db 30 LAALE 34

RESULT 23

O61645

ID O61645 PRELIMINARY; PRT; 39 AA.
AC O61645;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-tubulin (Fragment).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung Y.J., Zhu D.F., Ambron R.T.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF055329; AAC12647.1; -.
FT NON_TER 1 1

SQ SEQUENCE 39 AA; 4393 MW; 0D3A0EB30DFC29AF CRC64;

Query Match 12.8%; Score 5; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
 |||||
Db 12 LAALE 16

RESULT 24

Q9ZXK1

ID Q9ZXK1 PRELIMINARY; PRT; 39 AA.
AC Q9ZXK1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf24.5.
OS Bacteriophage phi CTX.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=35343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RA Hayashi T.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=99157549; PubMed=10027959;
RA Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;
RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
RT phage of Pseudomonas aeruginosa: implications for phage evolution and
RT horizontal gene transfer via bacteriophage.";
RL Mol. Microbiol. 31:399-419(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=90014160; PubMed=2507866;
RA Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
RT "Pseudomonas aeruginosa cytotoxin; the nucleotide sequence of the gene
RT and the mechanism of activation of the protoxin.";
RL Mol. Microbiol. 3:861-868(1989).
DR EMBL; AB008550; BAA36252.1; -.
SQ SEQUENCE 39 AA; 4587 MW; C9100CE65CF14BBE CRC64;

Query Match 12.8%; Score 5; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERAR 15
 |||||
Db 27 RERAR 31

RESULT 25

Q9ZRY5

ID Q9ZRY5 PRELIMINARY; PRT; 39 AA.
AC Q9ZRY5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoribosylpyrophosphate amidotransferase (Fragment).
GN PRAT.
OS Prunus avium (Cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitts H.B., Coutts R.H.A.;
RL Plant Mol. Biol. 40:531-531(1999).
DR EMBL; AJ011797; CAA09786.1; -.
KW Transferase.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4244 MW; 06343203D5C3778F CRC64;

Query Match 12.8%; Score 5; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||
Db 11 SLALA 15

RESULT 26

Q9PXW1

ID Q9PXW1 PRELIMINARY; PRT; 39 AA.
AC Q9PXW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE REV regulatory protein (Fragment).
OS Simian immunodeficiency virus SIVmac.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93276581; PubMed=7684879;
RA Benichou S., Venet A., Beyer C., Tiollais P., Madaule P.;
RT "Characterization of B-cell epitopes in the envelope glycoproteins of
RT simian immunodeficiency virus."
RL Virology 194:870-874(1993).
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
SQ SEQUENCE 39 AA; 4892 MW; CB1C6F359A3D037D CRC64;

Query Match 12.8%; Score 5; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALAD 6
|||||
Db 23 LALAD 27

RESULT 27

Q8F6J1

ID Q8F6J1 PRELIMINARY; PRT; 39 AA.
AC Q8F6J1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1315.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011311; AAN48514.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 39 AA; 4720 MW; 2E6008943ADC3BF9 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
|||||
Db 11 KLLVL 15

RESULT 28

Q8NHY1

ID Q8NHY1 PRELIMINARY; PRT; 28 AA.
AC Q8NHY1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hepatic nuclear factor 4 alpha (Fragment).
GN HNF4A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21592951; PubMed=11717395;
RA Boj S.F., Parrizas M., Maestro M.A., Ferrer J.;
RT "A transcription factor regulatory circuit in differentiated
pancreatic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14481-14486(2001).
RN [2]

RP SEQUENCE FROM N.A.
 RA Boj S.F., Parrizas M., Ferrer J.;
 RT "HNF4A expression in human pancreatic cells.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF509467; AAM34296.1; -.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3003 MW; 0F314BDCBC5D2958 CRC64;

Query Match 10.3%; Score 4; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERA 14
 ||||
 Db 15 RERA 18

RESULT 29

Q8MJG7

ID Q8MJG7 PRELIMINARY; PRT; 28 AA.
 AC Q8MJG7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Aldo-keto reductase family 1 member C2 (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nonneman D.J., Rohrer G.A.;
 RT "Comparative mapping of a region on chromosome 10q containing QTL for
 RT reproduction in swine.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF473815; AAM70050.1; -.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR Pfam; PF00248; aldo_ket_red; 1.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3008 MW; D319BA9C0D27F7A4 CRC64;

Query Match 10.3%; Score 4; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALE 21
 ||||
 Db 13 AALE 16

RESULT 30

Q95L33

ID Q95L33 PRELIMINARY; PRT; 28 AA.
 AC Q95L33;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Potassium chloride cotransporter SLC12A4 (Fragment).
 GN SLC12A4.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanzawa K., Lear T.L., Bailey E.;
 RT "Mapping of equine potassium chloride cotransporter (SLC12A4) and
 RT amino acid transporters (SLC7A10 and SLC7A9) and analysis for effect
 RT of polymorphism on osmotic fragility of red blood cells.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF425260; AAL18852.1; -.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3364 MW; F2D772124C232F5C CRC64;

Query Match 10.3%; Score 4; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
 ||||
 Db 12 LLVL 15

RESULT 31

P92760

ID P92760 PRELIMINARY; PRT; 28 AA.
 AC P92760;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit I (Fragment).
 GN ND1.
 OS Uromastix acanthinura.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
 OC Uromastix.
 OX NCBI_TaxID=52167;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 RT rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).

DR EMBL; U71325; AAC62247.1; -.

KW Mitochondrion.

FT NON_TER 1 1

SQ SEQUENCE 28 AA; 3057 MW; 4A37F11E5C4EEDAE CRC64;

Query Match 10.3%; Score 4; DB 8; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20

||||

Db 20 LAAL 23

RESULT 32

Q9QVC9

ID Q9QVC9 PRELIMINARY; PRT; 28 AA.

AC Q9QVC9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Glutathione S-transferase subunit YX, GST subunit YX (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=92231842; PubMed=1567376;

RA Igarashi T., Tsuchiya T., Shikata Y., Sagami F., Tagaya O., Horie T.,

RA Satoh T.;

RT "Developmental aspects of a unique glutathione S-transferase subunit

RT Yx in the liver cytosol from rats with hereditary hyperbilirubinuria.

RT Comparison with rat fetal liver transferase subunit Yfetus.";

RL Biochem. J. 283:307-311(1992).

DR HSSP; P24472; 1GUK.

DR InterPro; IPR004045; GST_Nterm.

DR Pfam; PF02798; GST_N; 1.

FT NON_TER 1 1

FT NON_TER 28 28

SQ SEQUENCE 28 AA; 3137 MW; 2C0CE25C09F0216F CRC64;

Query Match 10.3%; Score 4; DB 11; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19

||||

Db 21 LLAA 24

RESULT 33

Q62677

ID Q62677 PRELIMINARY; PRT; 28 AA.

AC Q62677; O09145; O09065;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-1 collagen type IV (Fragment).
GN COL4A1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97107443; PubMed=8950183;
RA Grande J.P., Melder D.C., Kluge D.L., Wieben E.D.;
RT "Structure of the rat collagen IV promoter."
RL Biochim. Biophys. Acta 1309:85-88(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Grande J.P., Haugen J.D.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U85606; AAB47426.1; -.
KW Collagen.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3113 MW; 96DFCAC741E07809 CRC64;

Query Match 10.3%; Score 4; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
| | | |
Db 13 LAAL 16

RESULT 34

Q8TGQ9

ID Q8TGQ9 PRELIMINARY; PRT; 29 AA.
AC Q8TGQ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 3.3 kDa protein.
GN YNL103W-A.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21624570; PubMed=11753363;
RA Kumar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
RA Miller P., Gerstein M.B., Snyder M.;
RT "An integrated approach for finding overlooked genes in yeast."
RL Nat. Biotechnol. 20:58-63(2002).
DR EMBL; AF479929; AAL79242.1; -.
KW Hypothetical protein.
SQ SEQUENCE 29 AA; 3350 MW; EC03E8528B54DF2E CRC64;

Query Match 10.3%; Score 4; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLV 35
||||
Db 26 KLLV 29

RESULT 35

Q9BR24

ID Q9BR24 PRELIMINARY; PRT; 29 AA.
AC Q9BR24;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ269M15.2 (Protein tyrosine phosphatase, receptor type, T (RPTPRHO,
DE KIAA0283)) (Fragment).
GN PTPRT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL021395; CAC24740.2; -.
KW Receptor.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2914 MW; AC6B6A4C94F4A38E CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
||||
Db 4 LAAL 7

RESULT 36

Q9UBW6

ID Q9UBW6 PRELIMINARY; PRT; 29 AA.
AC Q9UBW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DR beta-3 protein (Fragment).
GN HLA-DRB3\$0201 OR HLA-DRB3\$0101 OR HLA-DRB3\$0301.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93216303; PubMed=8462990;
RA Louis P., Eliaou J.F., Kerlan-Candon S., Pinet V., Vincent R.D.,

RA Clot J.;
 RT "Polymorphism in the regulatory region of HLA-DRB genes correlating
 RT with haplotype evolution."
 RL Immunogenetics 38:21-26(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kerlan-Candon S.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; X65559; CAA46529.1; -.
 DR EMBL; X65558; CAA46528.1; -.
 DR EMBL; X65560; CAA46530.1; -.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2951 MW; 2870A12FC80685DF CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
 ||||
 Db 12 LAAL 15

RESULT 37

Q9UCW5

ID Q9UCW5 PRELIMINARY; PRT; 29 AA.
 AC Q9UCW5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 11 beta-hydroxysteroid dehydrogenase type 2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96064773; PubMed=7593417;
 RA Wilson R.C., Harbison M.D., Krozowski Z.S., Funder J.W.,
 RA Shackleton C.H., Hanauske-Abel H.M., Wei J.Q., Hertecant J., Moran A.,
 RA Neiberger R.E.;
 RT "Several homozygous mutations in the gene for 11 beta-hydroxysteroid
 RT dehydrogenase type 2 in patients with apparent mineralocorticoid
 RT excess."
 RL J. Clin. Endocrinol. Metab. 80:3145-3150(1995).
 SQ SEQUENCE 29 AA; 3407 MW; CE826368D0714C00 CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
 ||||
 Db 5 LLAA 8

RESULT 38

Q9BM71

ID Q9BM71 PRELIMINARY; PRT; 29 AA.
AC Q9BM71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LINE-like reverse transcriptase (Fragment).
OS *Lasius niger*.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Formicinae; *Lasius*.
OX NCBI_TaxID=67767;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=LRT-L1 retrotransposon;
RX MEDLINE=20570504; PubMed=11121049;
RA Arkhipova I., Meselson M.;
RT "Transposable elements in sexual and ancient asexual taxa.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
DR EMBL; AY013922; AAG59907.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3060 MW; 6094F8E00837A336 CRC64;

Query Match 10.3%; Score 4; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LADD 7
|||
Db 18 LADD 21

RESULT 39

Q29891

ID Q29891 PRELIMINARY; PRT; 29 AA.
AC Q29891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA-DRB protein (Fragment).
GN HLA-DRB.
OS *Homo sapiens* (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; *Homo*.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93216303; PubMed=8462990;
RA Louis P., Eliaou J.F., Kerlan-Candon S., Pinet V., Vincent R.D.,
RA Clot J.;
RT "Polymorphism in the regulatory region of the HLA-DRB genes
RT correlating with ancestral haplotype evolution.";
RL Immunogenetics 38:21-26(1993).
DR EMBL; X65585; CAA46544.1; -.
FT NON_TER 29 29

SQ SEQUENCE 29 AA; 2952 MW; 287F87E8CB7AF5DF CRC64;

Query Match 10.3%; Score 4; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
||||
Db 26 LALA 29

RESULT 40

O19668

ID O19668 PRELIMINARY; PRT; 29 AA.
AC O19668;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA-DRB4\$0101 protein (Fragment).
GN HLA-DRB4\$0101.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Louis P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X65567; CAA46536.1; -.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2862 MW; 2860BAE8CB6685DF CRC64;

Query Match 10.3%; Score 4; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
||||
Db 26 LALA 29

Search completed: January 14, 2004, 10:42:28
Job time : 44.1589 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 6.43925 Seconds
 (without alignments)
 284.822 Million cell updates/sec

Title: US-09-843-221A-170
 Perfect score: 39
 Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	12.8	31	1	PETL_ARATH	P56776 arabidopsis
2	5	12.8	31	1	PETL_BETVU	P46612 beta vulgar
3	5	12.8	31	1	PETL_MAIZE	P19445 zea mays (m
4	5	12.8	31	1	PETL_OENHO	Q9mtk4 oenothera h
5	5	12.8	31	1	PETL_ORYSA	P12180 oryza sativ
6	5	12.8	31	1	PETL_PSINU	Q8wi03 psilotum nu
7	5	12.8	31	1	PETL_SPIOL	Q9m310 spinacia ol
8	5	12.8	31	1	PETL_TOBAC	P12181 nicotiana t
9	5	12.8	31	1	PETL_WHEAT	P58247 triticum ae
10	5	12.8	37	1	REV_SIVM2	P08809 simian immu
11	4	10.3	28	1	PA22_MICNI	P21791 micrurus ni
12	4	10.3	28	1	PETL_CYAPA	P48102 cyanophora
13	4	10.3	29	1	PETN_GUIITH	O78498 guillardia
14	4	10.3	29	1	PETN_ODOSI	P49527 odontella s
15	4	10.3	29	1	PETN_SKECO	O96807 skeletonema
16	4	10.3	31	1	PETN_CYACA	Q9t1r6 cyanidium c
17	4	10.3	31	1	PSAM_CHLVU	P56314 chlorella v

18	4	10.3	31	1	PSAM_SYNY3	P72986	synechocyst
19	4	10.3	32	1	PSBZ_EUGST	Q8sl89	euglena ste
20	4	10.3	33	1	PBAN_LYMDI	P43511	lymantria d
21	4	10.3	33	1	YC12_MARPO	P31560	marchantia
22	4	10.3	35	1	PETG_CYACA	Q9tlq9	cyanidium c
23	4	10.3	36	1	PYY_RAJRH	P29206	raja rhina
24	4	10.3	37	1	DIU1_TENMO	P56618	tenebrio mo
25	4	10.3	37	1	RK36_NEPOL	Q9tl26	nephroselmi
26	4	10.3	38	1	CPRP_CANPG	P81033	cancer pagu
27	4	10.3	39	1	GVPC_SPICC	P81000	spirulina s
28	4	10.3	39	1	NPF_MONEX	P41967	moniezia ex
29	4	10.3	39	1	PHRI_BACSU	O31492	bacillus su
30	4	10.3	40	1	THIO_CLOSG	P81108	clostridium
31	4	10.3	40	1	UC11_MAIZE	P80617	zea mays (m
32	3	7.7	28	1	CH60_MYCSM	P80673	mycobacteri
33	3	7.7	28	1	MAAI_RAT	P57113	rattus norv
34	3	7.7	28	1	OBP1_HYSCR	P81647	hystrix cri
35	3	7.7	28	1	ORND_PLAOR	P25513	placobdella
36	3	7.7	28	1	SMS2_ORENI	P81029	oreochromis
37	3	7.7	28	1	VIP_ALLMI	P48142	alligator m
38	3	7.7	28	1	VIP_DIDMA	P39089	didelphis m
39	3	7.7	28	1	VIP_RANRI	P81016	rana ridibu
40	3	7.7	28	1	VIP_SCYCA	P09685	scyliorhinu
41	3	7.7	28	1	VIP_SHEEP	P04565	ovis aries
42	3	7.7	28	1	Y16P_BPT4	P39248	bacterioph
43	3	7.7	29	1	ATP9_PICPJ	Q06838	pichia pijp
44	3	7.7	29	1	ATPA_BRYMA	P26965	bryopsis ma
45	3	7.7	29	1	CERB_CERCA	P36191	ceratitidis c
46	3	7.7	29	1	GALA_ALLMI	P47215	alligator m
47	3	7.7	29	1	GALA_AMICA	P47214	amia calva
48	3	7.7	29	1	GALA_CHICK	P30802	gallus gall
49	3	7.7	29	1	GALA_ONCMY	P47213	oncorhynch
50	3	7.7	29	1	GALA_RANRI	P47216	rana ridibu
51	3	7.7	29	1	GALA_SHEEP	P31234	ovis aries
52	3	7.7	29	1	HOXY_RHOOP	P22660	rhodococcus
53	3	7.7	29	1	HS98_NEUCR	P31540	neurospora
54	3	7.7	29	1	KDPF_ECOLI	P36937	escherichia
55	3	7.7	29	1	PETN_ANASP	Q9l3p6	anabaena sp
56	3	7.7	29	1	PETN_ARATH	P12178	arabidopsis
57	3	7.7	29	1	PETN_CYAPA	P48258	cyanophora
58	3	7.7	29	1	PETN_MAIZE	Q33302	zea mays (m
59	3	7.7	29	1	PETN_MARPO	P12177	marchantia
60	3	7.7	29	1	PETN_PINTH	P41611	pinus thunb
61	3	7.7	29	1	PETN_PORPU	P51276	porphyra pu
62	3	7.7	29	1	PETN_PSINU	Q8wi23	psilotum nu
63	3	7.7	29	1	PETN_SYNY3	P72717	synechocyst
64	3	7.7	29	1	PSAM_GUITH	O78448	guillardia
65	3	7.7	29	1	PSAX_SYNVU	P23320	synechococc
66	3	7.7	29	1	RP54_CLOKL	P38944	clostridium
67	3	7.7	29	1	SODC_OLEEU	P80740	olea europa
68	3	7.7	29	1	TL16_SPIOL	P81834	spinacia ol
69	3	7.7	29	1	Y15_BPT7	P03792	bacterioph
70	3	7.7	29	1	YCXC_ODOSI	P49838	odontella s
71	3	7.7	30	1	AATC_RABIT	P12343	oryctolagus
72	3	7.7	30	1	CALM_LYTPI	P05935	lytechinus
73	3	7.7	30	1	CIRA_CHAPA	P56871	chassalia p
74	3	7.7	30	1	CYO7_VIOOD	P58439	viola odora

75	3	7.7	30	1	DEF2_MACMU	P82317	macaca mula
76	3	7.7	30	1	DMS3_PHYSA	P80279	phyllomedus
77	3	7.7	30	1	FMBB_BACNO	P17829	bacteroides
78	3	7.7	30	1	HETA_RADMA	P58691	radianthus
79	3	7.7	30	1	ITI1_LAGLE	P26771	lagenaria l
80	3	7.7	30	1	ITR1_CITLA	P11969	citrullus l
81	3	7.7	30	1	ITR1_MOMCH	P10294	momordica c
82	3	7.7	30	1	OTCC_AERPU	P11726	aeromonas p
83	3	7.7	30	1	PCG1_PACGO	P82414	pachycondyl
84	3	7.7	30	1	PCG2_PACGO	P82415	pachycondyl
85	3	7.7	30	1	PCG3_PACGO	P82416	pachycondyl
86	3	7.7	30	1	PMGY_CANAL	P82612	candida alb
87	3	7.7	30	1	PRT1_CLUPA	P02335	clupea pall
88	3	7.7	30	1	PSAM_MESVI	Q9mus2	mesostigma
89	3	7.7	30	1	PSAM_ODOSI	P49487	odontella s
90	3	7.7	30	1	RIPS_MOMCO	P20655	momordica c
91	3	7.7	30	1	RL18_HALCU	P05970	halobacteri
92	3	7.7	30	1	SDHA_CLOPR	P80212	clostridium
93	3	7.7	30	1	UP62_UPEIN	P82038	uperoleia i
94	3	7.7	30	1	URE1_ECOLI	Q03284	escherichia
95	3	7.7	30	1	VATN_BOVIN	P81134	bos taurus
96	3	7.7	30	1	VG03_BPPF1	P25137	bacterioph
97	3	7.7	30	1	Y425_BORBU	O51386	borrelia bu
98	3	7.7	30	1	Y523_BORBU	O51473	borrelia bu
99	3	7.7	30	1	Y573_TREPA	O83583	treponema p
100	3	7.7	30	1	YCCB_ECOLI	P24244	escherichia
101	3	7.7	31	1	BCAM_PIG	O19098	sus scrofa
102	3	7.7	31	1	CTRP_PENMO	P35002	penaeus mon
103	3	7.7	31	1	CU54_LOCFI	P11738	locusta mig
104	3	7.7	31	1	DIUX_DIPPU	P82372	diploptera
105	3	7.7	31	1	HBA_MACEU	P81043	macropus eu
106	3	7.7	31	1	HCY1_HOMAM	P82296	homarus ame
107	3	7.7	31	1	HCY2_MAISQ	P82303	maia squina
108	3	7.7	31	1	LPL_BUCRP	Q53017	buchnera ap
109	3	7.7	31	1	PETL_ANASP	Q8yvq2	anabaena sp
110	3	7.7	31	1	PETL_GUIITH	O78468	guillardia
111	3	7.7	31	1	PETL_LOTJA	Q9bbr4	lotus japon
112	3	7.7	31	1	PETL_MARPO	P12179	marchantia
113	3	7.7	31	1	PETL_MESVI	Q9mun4	mesostigma
114	3	7.7	31	1	PETL_NEPOL	Q9tky9	nephroselmi
115	3	7.7	31	1	PETL_ODOSI	P49524	odontella s
116	3	7.7	31	1	PETL_POPDE	O20272	populus del
117	3	7.7	31	1	PETM_CYACA	Q9tlr5	cyanidium c
118	3	7.7	31	1	PRT2_CLUPA	P02336	clupea pall
119	3	7.7	31	1	PSAM_CYAPA	P48185	cyanophora
120	3	7.7	31	1	PSAM_EUGGR	P31479	euglena gra
121	3	7.7	31	1	PSAM_SYNEL	P25903	synechococc
122	3	7.7	31	1	PSBK_SYNVU	P19054	synechococc
123	3	7.7	31	1	PSBM_MESVI	Q9muq7	mesostigma
124	3	7.7	31	1	PSBT_CHLRE	P37256	chlamydomon
125	3	7.7	31	1	PSBT_CHLVU	P56327	chlorella v
126	3	7.7	31	1	PSBT_CYAPA	P48109	cyanophora
127	3	7.7	31	1	PSBT_EUGGR	P20176	euglena gra
128	3	7.7	31	1	PSBT_MESVI	Q9muv6	mesostigma
129	3	7.7	31	1	PSBT_PORPU	P51323	porphyra pu
130	3	7.7	31	1	PYSG_METBA	P80523	methanosarc
131	3	7.7	31	1	RECX_METCL	P37865	methylomona

132	3	7.7	31	1	SARL_HUMAN	O00631	homo sapien
133	3	7.7	31	1	SARL_MOUSE	Q9cqd6	mus musculu
134	3	7.7	31	1	SARL_RABIT	P42532	oryctolagus
135	3	7.7	31	1	Y3KD_BPCHP	P19187	bacteriopha
136	3	7.7	32	1	ADHR_DROYA	P28487	drosophila
137	3	7.7	32	1	APL3_DIAGR	P81471	diatraea gr
138	3	7.7	32	1	B4G1_RAT	P80225	r beta-1,4-
139	3	7.7	32	1	CAL2_ONCKE	P01264	oncorhynchu
140	3	7.7	32	1	CAL3_ONCKI	P01265	oncorhynchu
141	3	7.7	32	1	CAL_ANGJA	P01262	anguilla ja
142	3	7.7	32	1	CAPP_METEX	Q49136	methylobact
143	3	7.7	32	1	CYBL_RHOGR	P32953	rhodotorula
144	3	7.7	32	1	DBH_SYNY1	P02343	synechocyst
145	3	7.7	32	1	FER_PORCR	P18821	porphyridiu
146	3	7.7	32	1	IAPP_SAGOE	Q28934	saguinus oe
147	3	7.7	32	1	LPID_ECOLI	P03060	escherichia
148	3	7.7	32	1	LPID_EDWTA	P08140	edwardsiell
149	3	7.7	32	1	LPIV_ECOLI	P03061	escherichia
150	3	7.7	32	1	PETM_PORPU	P51275	porphyra pu
151	3	7.7	32	1	PRI3_ONCMY	P02330	oncorhynchu
152	3	7.7	32	1	PRT7_ONCMY	P08146	oncorhynchu
153	3	7.7	32	1	PRT8_ONCMY	P12817	oncorhynchu
154	3	7.7	32	1	PRT_ORYLA	Q91185	oryzias lat
155	3	7.7	32	1	PSAM_MARPO	P31590	marchantia
156	3	7.7	32	1	PSBQ_PEA	P19589	pisum sativ
157	3	7.7	32	1	PSBT_ODOSI	P49516	odontella s
158	3	7.7	32	1	PSBZ_EUGAN	Q8sl95	euglena ana
159	3	7.7	32	1	PSBZ_EUGGA	Q8sl93	euglena gra
160	3	7.7	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
161	3	7.7	32	1	Y16O_BPT4	P39247	bacteriopha
162	3	7.7	32	1	Y433_BORBU	O51394	borrelia bu
163	3	7.7	32	1	YCPG_MASLA	P29735	mastigoclad
164	3	7.7	32	1	YTK3_ILTVT	P23985	infectious
165	3	7.7	33	1	ALOX_PICPA	P04842	pichia past
166	3	7.7	33	1	ANP3_MYOSC	P04367	myoxocephal
167	3	7.7	33	1	ANP5_MYOAE	P20421	myoxocephal
168	3	7.7	33	1	DEF1_MESAU	P81465	mesocricetu
169	3	7.7	33	1	DEF3_MESAU	P81467	mesocricetu
170	3	7.7	33	1	FER_PORAE	P18820	porphyridiu
171	3	7.7	33	1	MBP1_MAIZE	P28794	zea mays (m
172	3	7.7	33	1	PETM_SYNEL	Q8dj15	synechococc
173	3	7.7	33	1	PK1_DICDI	P34101	dictyosteli
174	3	7.7	33	1	PRTB_MUGCE	P08130	mugil cepha
175	3	7.7	33	1	PRTL_ECOLI	P02338	escherichia
176	3	7.7	33	1	PSBT_ARATH	P37259	arabidopsis
177	3	7.7	33	1	PSBT_MAIZE	P37257	zea mays (m
178	3	7.7	33	1	RL4_HALCU	P05967	halobacteri
179	3	7.7	33	1	RPOC_HETCA	P36441	heterosigma
180	3	7.7	33	1	Y474_BORBU	O51430	borrelia bu
181	3	7.7	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
182	3	7.7	33	1	YC12_CHLRE	P50370	chlamydomon
183	3	7.7	33	1	YC12_MESVI	Q9mus3	mesostigma
184	3	7.7	34	1	COL_CHICK	P11148	gallus gall
185	3	7.7	34	1	COXA_THETH	P82543	thermus the
186	3	7.7	34	1	DEF2_RABIT	P07468	oryctolagus
187	3	7.7	34	1	DMS1_PHYSA	P24302	phyllomedus
188	3	7.7	34	1	DMS2_PHYSA	P80278	phyllomedus

189	3	7.7	34	1	HEMO_CHICK	P20057	gallus gall
190	3	7.7	34	1	MYTB_MYTED	P81613	mytilus edu
191	3	7.7	34	1	PETM_ANASP	Q9f4w2	anabaena sp
192	3	7.7	34	1	PRT1_SCOSC	P83264	scomber sco
193	3	7.7	34	1	PRT2_SCOSC	P83265	scomber sco
194	3	7.7	34	1	PRT_DICLA	Q9ps27	dicentrarch
195	3	7.7	34	1	PRT_PERFV	P29629	perca flave
196	3	7.7	34	1	PSBT_TOBAC	P12184	nicotiana t
197	3	7.7	34	1	PSPC_BOVIN	P15783	bos taurus
198	3	7.7	34	1	PSPC_CANFA	P22397	canis famil
199	3	7.7	34	1	RR2_OCHNE	Q40606	ochrosphaer
200	3	7.7	34	1	SMS_MYXGL	P19209	myxine glut
201	3	7.7	34	1	VLYS_BPM1	P08229	bacterioph
202	3	7.7	34	1	VPU_HV1W2	P08808	human immun
203	3	7.7	34	1	Y870_HAEIN	P44065	haemophilus
204	3	7.7	34	1	YC12_GUIITH	O78460	guillardia
205	3	7.7	34	1	YC12_ODOSI	P49529	odontella s
206	3	7.7	34	1	YC12_SKECO	O96797	skeletonema
207	3	7.7	35	1	ADO1_AGRDO	P58608	agriosphodr
208	3	7.7	35	1	ERFK_KLEAE	Q08599	klebsiella
209	3	7.7	35	1	EXE2_HELUS	P04204	heloderma s
210	3	7.7	35	1	NEF_HV1H3	P05854	human immun
211	3	7.7	35	1	PBP2_LYMDI	P34177	lymantria d
212	3	7.7	35	1	PSBT_MARPO	P12182	marchantia
213	3	7.7	35	1	PSBT_OENHO	P37258	oenothera h
214	3	7.7	35	1	PSBT_ORYSA	P12183	oryza sativ
215	3	7.7	35	1	PSBT_PINTH	P41625	pinus thunb
216	3	7.7	35	1	PSPC_PIG	P15785	sus scrofa
217	3	7.7	35	1	RL15_SYNP7	P31160	synechococc
218	3	7.7	35	1	RL32_HALCU	P05965	halobacteri
219	3	7.7	35	1	SMS_LAMFL	Q9prro	lampetra fl
220	3	7.7	35	1	TX1_THRPR	P83480	thrixopelma
221	3	7.7	35	1	WSP7_PINPS	P81086	pinus pinas
222	3	7.7	35	1	YC12_CYACA	Q9tlx0	cyanidium c
223	3	7.7	35	1	YQB5_CAEEL	Q09258	caenorhabdi
224	3	7.7	36	1	AMPL_PIG	P28839	sus scrofa
225	3	7.7	36	1	CECD_ANTPE	P01511	antheraea p
226	3	7.7	36	1	ELH_THETS	P80594	theromyzon
227	3	7.7	36	1	HBB_PONPY	Q9tt34	pongo pygma
228	3	7.7	36	1	LYOX_PIG	P45845	sus scrofa
229	3	7.7	36	1	MPG2_DACGL	Q41183	dactylis gl
230	3	7.7	36	1	MYPC_RAT	P56741	rattus norv
231	3	7.7	36	1	NEUH_CARCA	P11975	cardisoma c
232	3	7.7	36	1	NEUY_GADMO	P80167	gadus morhu
233	3	7.7	36	1	NEUY_ONCMY	P29071	oncorhynch
234	3	7.7	36	1	NEUY_RABIT	P09640	oryctolagus
235	3	7.7	36	1	NEUY_RANRI	P29949	rana ridibu
236	3	7.7	36	1	NIFH_ENTAG	P26249	enterobacte
237	3	7.7	36	1	NUCM_SOLTU	P80264	solanum tub
238	3	7.7	36	1	OSTS_YEAST	Q99380	saccharomyc
239	3	7.7	36	1	PAHO_ANSAN	P06304	anser anser
240	3	7.7	36	1	PAHO_DIDMA	P18107	didelphis m
241	3	7.7	36	1	PAHO_LARAR	P41337	larus argen
242	3	7.7	36	1	PAHO_RABIT	P41336	oryctolagus
243	3	7.7	36	1	PAHO_STRCA	P11967	struthio ca
244	3	7.7	36	1	PSAD_PEA	P20117	pisum sativ
245	3	7.7	36	1	PSAH_PEA	P20121	pisum sativ

246	3	7.7	36	1	PSAI_SKECO	096813	skeletonema
247	3	7.7	36	1	PSBY_ODOSI	P49543	odontella s
248	3	7.7	36	1	PSBY_PORPU	P51206	porphyra pu
249	3	7.7	36	1	PYY_AMICA	P29205	amia calva
250	3	7.7	36	1	PYY_LEPSP	P09473	lepisosteus
251	3	7.7	36	1	PYY_ONCKI	P09474	oncorhynchus
252	3	7.7	36	1	R18A_BOVIN	P82919	bos taurus
253	3	7.7	36	1	Y297_ARCFU	O29945	archaeoglob
254	3	7.7	36	1	Y699_TREPA	O83697	treponema p
255	3	7.7	36	1	YC12_CYAPA	P48256	cyanophora
256	3	7.7	37	1	24KD_PLACH	P14592	plasmodium
257	3	7.7	37	1	ANP3_PSEAM	P02733	pseudopleur
258	3	7.7	37	1	CALR_RANRI	P31888	rana ridibu
259	3	7.7	37	1	CEC2_MANSE	P14662	manduca sex
260	3	7.7	37	1	CEC3_MANSE	P14663	manduca sex
261	3	7.7	37	1	CEC4_MANSE	P14664	manduca sex
262	3	7.7	37	1	GHR3_RAT	P33580	rattus norv
263	3	7.7	37	1	HCYB_CANPG	P83175	cancer pagu
264	3	7.7	37	1	HOXF_RHOOP	P22658	rhodococcus
265	3	7.7	37	1	ME20_EUPRA	P26888	euplotes ra
266	3	7.7	37	1	OGT1_RABIT	P81436	oryctolagus
267	3	7.7	37	1	PETG_PORPU	P51318	porphyra pu
268	3	7.7	37	1	PETG_SKECO	O96811	skeletonema
269	3	7.7	37	1	PSBY_GUITH	O78433	guillardia
270	3	7.7	37	1	PYY_CHICK	P29203	gallus gall
271	3	7.7	37	1	RK36_ASTLO	P24355	astasia lon
272	3	7.7	37	1	RK36_EUGGR	P21532	euglena gra
273	3	7.7	37	1	RK36_PEA	P07815	pisum sativ
274	3	7.7	37	1	RK36_PORPU	P51296	porphyra pu
275	3	7.7	37	1	RL36_DEIRA	Q9rsk0	deinococcus
276	3	7.7	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
277	3	7.7	37	1	RL36_MYCTU	P45810	mycobacteri
278	3	7.7	37	1	RL36_STRCO	O86772	streptomyce
279	3	7.7	37	1	RL36_THETH	P80256	thermus the
280	3	7.7	37	1	SMS_PETMA	P21779	petromyzon
281	3	7.7	37	1	TCTP_TRYBB	P35758	trypanosoma
282	3	7.7	37	1	THHS_HORVU	P33045	hordeum vul
283	3	7.7	37	1	VG65_BPPH2	P16515	bacterioph
284	3	7.7	37	1	VG65_BPPZA	P08384	bacterioph
285	3	7.7	37	1	VGJ_BPPHX	P03651	bacterioph
286	3	7.7	37	1	VPU_HV1Z8	P08807	human immun
287	3	7.7	37	1	Y63_BPT3	P20328	bacterioph
288	3	7.7	37	1	YBGT_ECOLI	P56100	escherichia
289	3	7.7	37	1	YC12_CHLVU	P56328	chlorella v
290	3	7.7	37	1	YIM4_BPPH1	P10428	bacterioph
291	3	7.7	37	1	YRYL_CAEEL	Q19177	caenorhabdi
292	3	7.7	38	1	EXE1_HELSU	P04203	heloderma s
293	3	7.7	38	1	GME1_RAT	Q9quz8	rattus norv
294	3	7.7	38	1	MUTS_YEREN	P47763	yersinia en
295	3	7.7	38	1	NLT1_VITSX	P80275	vitis sp. (
296	3	7.7	38	1	NLT2_VITSX	P33556	vitis sp. (
297	3	7.7	38	1	PACA_URAJA	P81039	uranoscopu
298	3	7.7	38	1	PSAI_ODOSI	P49484	odontella s
299	3	7.7	38	1	PSAI_SYNP2	Q54752	synechococc
300	3	7.7	38	1	PSBT_WHEAT	P37260	triticum ae
301	3	7.7	38	1	PSBX_ODOSI	P49509	odontella s
302	3	7.7	38	1	RL7_VIBCO	P05395	vibrio cost

303	3	7.7	38	1	TRPD_SERMA	P12321	serratia ma
304	3	7.7	38	1	VCOM_BPD10	Q38200	bacterioph
305	3	7.7	38	1	Y114_HAEIN	P43944	haemophilus
306	3	7.7	39	1	COL_SQUAC	P11149	squalus aca
307	3	7.7	39	1	FUC3_RAT	P80349	rattus norv
308	3	7.7	39	1	GDLO_DROME	Q9u5v6	drosophila
309	3	7.7	39	1	GLT2_WHEAT	P02862	triticum ae
310	3	7.7	39	1	H2A_BUFBG	P55897	bufo bufo g
311	3	7.7	39	1	LIMB_XENLA	P37138	xenopus lae
312	3	7.7	39	1	PHRF_BACSU	P71001	bacillus su
313	3	7.7	39	1	PRT1_BUFJA	P24641	bufo japoni
314	3	7.7	39	1	PRT2_BUFJA	P24642	bufo japoni
315	3	7.7	39	1	PSBI_SYNP6	P17747	synechococc
316	3	7.7	39	1	PSBJ_GUIITH	O78463	guillardia
317	3	7.7	39	1	PSBL_SYNY3	Q55354	synechocyst
318	3	7.7	39	1	PSBX_CYAPA	P48266	cyanophora
319	3	7.7	39	1	PSBX_GUIITH	O78455	guillardia
320	3	7.7	39	1	PSBX_PORPU	P51197	porphyra pu
321	3	7.7	39	1	PSI1_PSEFL	P80694	pseudomonas
322	3	7.7	39	1	SYS_RABIT	P13642	oryctolagus
323	3	7.7	39	1	VCOM_HAEIN	P71390	haemophilus
324	3	7.7	39	1	VLYS_BPOX2	P08230	bacterioph
325	3	7.7	39	1	Y759_TREPA	O83740	treponema p
326	3	7.7	39	1	YU07_BORBU	O54572	borrelia bu
327	3	7.7	40	1	ALB1_TRASC	P81188	trachemys s
328	3	7.7	40	1	ANP8_MYOAE	P20617	myoxocephal
329	3	7.7	40	1	CH60_SOLTU	P80502	solanum tub
330	3	7.7	40	1	EST4_DROMO	P10094	drosophila
331	3	7.7	40	1	GKBL_GINBI	P83171	ginkgo bilo
332	3	7.7	40	1	GP55_BPSP1	O48409	bacterioph
333	3	7.7	40	1	HPT_RABIT	P19007	oryctolagus
334	3	7.7	40	1	PHAC_MASLA	P11389	mastigoclad
335	3	7.7	40	1	PHRC_BACSU	P94416	bacillus su
336	3	7.7	40	1	PHRK_BACSU	O31840	bacillus su
337	3	7.7	40	1	PSAI_PEA	P17227	pisum sativ
338	3	7.7	40	1	PSAJ_CYAPA	P48117	cyanophora
339	3	7.7	40	1	PSBJ_CYAPA	P19155	cyanophora
340	3	7.7	40	1	PTSA_LACLA	Q04938	lactococcus
341	3	7.7	40	1	RRPO_LSV	P27328	lily sympto
342	3	7.7	40	1	SAUV_PHYSA	P01144	phyllomedus
343	3	7.7	40	1	Y41_BPT7	P03782	bacterioph
344	3	7.7	40	1	YC04_ARCFU	O29064	archaeoglob
345	3	7.7	40	1	YC67_ARCFU	O29001	archaeoglob
346	3	7.7	40	1	YH76_ARCFU	O28498	archaeoglob
347	3	7.7	40	1	YSXC_SULAC	P39477	sulfolobus
348	2	5.1	28	1	ACON_CANAL	P82611	candida alb
349	2	5.1	28	1	APC1_RABIT	P33047	oryctolagus
350	2	5.1	28	1	ARYA_PSEPU	P35902	pseudomonas
351	2	5.1	28	1	ARYC_NOCGL	P80008	nocardia gl
352	2	5.1	28	1	COXB_SOLTU	P80499	solanum tub
353	2	5.1	28	1	ETX2_BACCE	P80568	bacillus ce
354	2	5.1	28	1	FIBA_CANFA	P02673	canis famil
355	2	5.1	28	1	GDO_TRIMO	P02865	triticum mo
356	2	5.1	28	1	GRP_ALLMI	P31886	alligator m
357	2	5.1	28	1	GTS5_CHICK	P20137	gallus gall
358	2	5.1	28	1	GUN_SCHCO	P81190	schizophyll
359	2	5.1	28	1	GVPC_OSCAG	P80999	oscillatori

360	2	5.1	28	1	HORC_HORSP	P02864	hordeum spo
361	2	5.1	28	1	HSP4_OCTVU	P83216	octopus vul
362	2	5.1	28	1	ICPP_VIPLE	P82475	vipera lebe
363	2	5.1	28	1	IEL1_MOMCH	P10296	momordica c
364	2	5.1	28	1	IORB_METTM	P80911	methanobact
365	2	5.1	28	1	ITR3_LUFCY	P35628	luffa cylin
366	2	5.1	28	1	LECA_IRIHO	P36230	iris hollan
367	2	5.1	28	1	LPFS_ECOLI	P22183	escherichia
368	2	5.1	28	1	LPL_ECOLI	P09149	escherichia
369	2	5.1	28	1	LPL_SALTI	Q8z9h9	salmonella
370	2	5.1	28	1	LPL_SALTY	P03062	salmonella
371	2	5.1	28	1	LPW_SERMA	P03055	serratia ma
372	2	5.1	28	1	MT2_BRANA	Q96353	brassica na
373	2	5.1	28	1	NLT2_WHEAT	P39085	triticum ae
374	2	5.1	28	1	OMPA_YERPS	P38399	yersinia ps
375	2	5.1	28	1	OST1_CHICK	P80896	gallus gall
376	2	5.1	28	1	PA23_TRIST	P82894	trimeresuru
377	2	5.1	28	1	PHR_METTM	P58818	methanobact
378	2	5.1	28	1	PHYB_ASPFI	P81440	aspergillus
379	2	5.1	28	1	PP71_HCMVT	P24429	human cytom
380	2	5.1	28	1	PPOX_BOVIN	P56602	bos taurus
381	2	5.1	28	1	RIP_PLETU	P83245	pleurotus t
382	2	5.1	28	1	RL5_HALCU	P05972	halobacteri
383	2	5.1	28	1	RS19_PHYS1	O66093	phytoplasma
384	2	5.1	28	1	SCX2_BUTSI	P15230	buthus sind
385	2	5.1	28	1	SLP1_LEIQH	P80669	leiurus qui
386	2	5.1	28	1	TXO2_AGEAP	P15971	agelenopsis
387	2	5.1	28	1	UC05_MAIZE	P80611	zea mays (m
388	2	5.1	28	1	VAO_PLEOS	P21800	pleurotus o
389	2	5.1	28	1	VG9_SPV4	P11341	spiroplasma
390	2	5.1	28	1	VI03_VACCP	Q00334	vaccinia vi
391	2	5.1	28	1	Y073_ARCFU	O30163	archaeoglob
392	2	5.1	28	1	YA79_ARCFU	O29184	archaeoglob
393	2	5.1	29	1	28KD_TRIFO	P33405	tritrichomo
394	2	5.1	29	1	AL21_HORSE	P81216	equus cabal
395	2	5.1	29	1	AMEL_RABIT	P12761	oryctolagus
396	2	5.1	29	1	BR2D_RANES	P40840	rana escule
397	2	5.1	29	1	BREE_RANES	P40841	rana escule
398	2	5.1	29	1	COA1_BPI22	P15413	bacterioph
399	2	5.1	29	1	COXJ_CANFA	Q9tr29	canis famil
400	2	5.1	29	1	COXK_SHEEP	Q9tr28	ovis aries
401	2	5.1	29	1	CU36_LOCMI	P11737	locusta mig
402	2	5.1	29	1	CXD6_CONGL	Q9twm7	conus glori
403	2	5.1	29	1	CXO7_CONGE	P05483	conus geogr
404	2	5.1	29	1	CXOC_CONMA	P37300	conus magus
405	2	5.1	29	1	DMD_RAT	P11530	rattus norv
406	2	5.1	29	1	DMS5_PHYSA	P80281	phyllomedus
407	2	5.1	29	1	GLUC_ANAPL	P01276	anas platyr
408	2	5.1	29	1	GLUC_CALMI	P13189	callorhynch
409	2	5.1	29	1	GLUC_CHIBR	P31297	chinchilla
410	2	5.1	29	1	GLUC_DIDMA	P18108	didelphis m
411	2	5.1	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
412	2	5.1	29	1	GLUC_PLAFE	P23062	platichthys
413	2	5.1	29	1	GLUC_RABIT	P25449	oryctolagus
414	2	5.1	29	1	GLUC_TORMA	P09567	torpedo mar
415	2	5.1	29	1	H2B2_ECHES	P13282	echinus esc
416	2	5.1	29	1	HRJ_BOTJA	P20416	bothrops ja

417	2	5.1	29	1	IPYR_DESVH	P19371	desulfovibr
418	2	5.1	29	1	ITH3_BOVIN	P56652	bos taurus
419	2	5.1	29	1	ITR1_CUCMA	P01074	cucurbita m
420	2	5.1	29	1	ITR1_LUFCY	P25849	luffa cylin
421	2	5.1	29	1	ITR1_MOMRE	P17680	momordica r
422	2	5.1	29	1	ITR2_BRYDI	P11968	bryonia dio
423	2	5.1	29	1	ITR3_CYCPE	P83394	cyclanthera
424	2	5.1	29	1	ITR4_CYCPE	P83395	cyclanthera
425	2	5.1	29	1	ITR5_CYCPE	P83396	cyclanthera
426	2	5.1	29	1	MDH_BURPS	P80536	burkholderi
427	2	5.1	29	1	MULR_ECHML	P81798	echis multi
428	2	5.1	29	1	NUO1_SOLTU	P80267	solanum tub
429	2	5.1	29	1	P2SM_LOXIN	P83046	loxosceles
430	2	5.1	29	1	PCG4_PACGO	P82417	pachycondyl
431	2	5.1	29	1	PETN_CHAGL	Q8ma13	chaetosphae
432	2	5.1	29	1	PETN_MESVI	Q9mus4	mesostigma
433	2	5.1	29	1	PETN_SYNEL	Q8dkn2	synechococc
434	2	5.1	29	1	PK4_DICDI	P34103	dictyosteli
435	2	5.1	29	1	PRO1_DACGL	P18689	dactylis gl
436	2	5.1	29	1	PSAF_SYNP6	P31083	synechococc
437	2	5.1	29	1	PSBI_SYNVU	P12240	synechococc
438	2	5.1	29	1	RL15_HALCU	P05971	halobacteri
439	2	5.1	29	1	RL15_STRLI	P49975	streptomyce
440	2	5.1	29	1	RS7_METTE	O93639	methanosarc
441	2	5.1	29	1	SLP2_LEIQH	P80670	leiurus qui
442	2	5.1	29	1	SLP3_LEIQH	P80671	leiurus qui
443	2	5.1	29	1	TLP_ACTDE	P81370	actinidia d
444	2	5.1	29	1	UN23_CLOPA	P81356	clostridium
445	2	5.1	29	1	Y51_BPT3	P20326	bacterioph
446	2	5.1	29	1	YCX4_ODOSI	P49830	odontella s
447	2	5.1	30	1	2ENR_CLOTY	P11887	clostridium
448	2	5.1	30	1	A1AT_CHIVI	P38026	chinchilla
449	2	5.1	30	1	AATM_RABIT	P12345	oryctolagus
450	2	5.1	30	1	ACB1_DIGLA	P81624	digitalis l
451	2	5.1	30	1	AMPT_BACST	P00728	bacillus st
452	2	5.1	30	1	ANF_RANRI	P09196	rana ridibu
453	2	5.1	30	1	CBAL_BACST	P13722	bacillus st
454	2	5.1	30	1	CH60_CLOPA	P81339	clostridium
455	2	5.1	30	1	CLPA_PINPS	P81671	pinus pinas
456	2	5.1	30	1	COAE_CORAM	P58101	corynebacte
457	2	5.1	30	1	COXC_SOLTU	P80500	solanum tub
458	2	5.1	30	1	CX2A_CONBE	P58625	conus betul
459	2	5.1	30	1	CXEX_CONCN	P58928	conus conso
460	2	5.1	30	1	CXK4_CONST	P58921	conus stria
461	2	5.1	30	1	CXOB_CONPE	P56713	conus penna
462	2	5.1	30	1	CXVA_CONER	P58782	conus ermin
463	2	5.1	30	1	CXVB_CONER	P58783	conus ermin
464	2	5.1	30	1	CY35_DESAC	P81079	desulphuromo
465	2	5.1	30	1	CYO1_VIOOD	P82230	viola odora
466	2	5.1	30	1	DIDH_COMTE	P80702	comamonas t
467	2	5.1	30	1	DIU2_HYLLI	P82015	hyles linea
468	2	5.1	30	1	DIU2_MANSE	P24858	manduca sex
469	2	5.1	30	1	END2_ONCKE	P01205	oncorhynch
470	2	5.1	30	1	FIBR_PANIN	P22775	panulirus i
471	2	5.1	30	1	FTN_BACFR	P28733	bacteroides
472	2	5.1	30	1	GLUM_ANGAN	P41521	anguilla an
473	2	5.1	30	1	HCY2_HOMAM	P82297	homarus ame

474	2	5.1	30	1	HSP5_OCTVU	P83217	octopus vul
475	2	5.1	30	1	HYP4_HYBPA	P58445	hybanthus p
476	2	5.1	30	1	IHFB_RHILE	P80606	rhizobium l
477	2	5.1	30	1	ITR2_ECBEL	P12071	ecballium e
478	2	5.1	30	1	ITR2_LUFYC	P25850	luffa cylin
479	2	5.1	30	1	ITR3_CUCMC	P32041	cucumis mel
480	2	5.1	30	1	ITR3_MOMCO	P82410	momordica c
481	2	5.1	30	1	ITR4_CUCSA	P10292	cucumis sat
482	2	5.1	30	1	ITR6_CYCPE	P83397	cyclanthera
483	2	5.1	30	1	ITR7_CYCPE	P83398	cyclanthera
484	2	5.1	30	1	KAB5_OLDAF	P58456	oldenlandia
485	2	5.1	30	1	LAS1_PIG	P80171	sus scrofa
486	2	5.1	30	1	LEAH_PHAVU	P81870	phaseolus v
487	2	5.1	30	1	MDH_HELGE	P80037	heliobacter
488	2	5.1	30	1	MMAL_DERMI	P16312	dermatophag
489	2	5.1	30	1	NU5M_PISOC	P24999	pisaster oc
490	2	5.1	30	1	NUO2_SOLTU	P80268	solanum tub
491	2	5.1	30	1	P2CO_ARTSP	P37365	arthrobacte
492	2	5.1	30	1	PCCA_MYXXA	P81185	myxococcus
493	2	5.1	30	1	PCG5_PACGO	P82418	pachycondyl
494	2	5.1	30	1	PETN_NEPOL	Q9t101	nephroselmi
495	2	5.1	30	1	PLF4_RABIT	P83470	oryctolagus
496	2	5.1	30	1	PLMS_SQUAC	P82542	squalus aca
497	2	5.1	30	1	PRT2_ONCMY	P02331	oncorhynchu
498	2	5.1	30	1	PRT3_ONCMY	P02332	oncorhynchu
499	2	5.1	30	1	PRT4_ONCMY	P02333	oncorhynchu
500	2	5.1	30	1	PRTB_ONCMY	P12819	oncorhynchu
501	2	5.1	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
502	2	5.1	30	1	PSAM_PINTH	P41601	pinus thunb
503	2	5.1	30	1	PSAM_PORPU	P51395	porphyra pu
504	2	5.1	30	1	PYSD_METBA	P80524	methanosarc
505	2	5.1	30	1	RKGG_LEPKE	P21587	lepidochely
506	2	5.1	30	1	RNP_ODOVI	P19640	odocoileus
507	2	5.1	30	1	SCK2_TITSE	P08816	tityus serr
508	2	5.1	30	1	SCX2_CENLI	P18927	centruroide
509	2	5.1	30	1	SILU_RHIPU	P02885	rhizomucor
510	2	5.1	30	1	TL29_SPIOL	P81833	spinacia ol
511	2	5.1	30	1	TX2_HETVE	P58426	heteropoda
512	2	5.1	30	1	TX2_THRPR	P83476	thrixopelma
513	2	5.1	30	1	UC35_MAIZE	P80641	zea mays (m
514	2	5.1	30	1	UDDP_SULAC	P80143	sulfolobus
515	2	5.1	30	1	UP61_UPEIN	P82037	uperoleia i
516	2	5.1	30	1	VAA1_EQUAR	Q04236	equisetum a
517	2	5.1	30	1	VAA1_PSINU	Q04237	psilotum nu
518	2	5.1	30	1	VAA2_EQUAR	Q04238	equisetum a
519	2	5.1	30	1	VAA2_PSINU	Q04239	psilotum nu
520	2	5.1	30	1	VPU_HV1SC	P05948	human immun
521	2	5.1	30	1	VTTA_BPT3	P20837	bacterioph
522	2	5.1	30	1	Y161_TREPA	O83196	treponema p
523	2	5.1	30	1	Y357_BORBU	O51332	borrelia bu
524	2	5.1	30	1	Y932_TREPA	O83902	treponema p
525	2	5.1	31	1	A98A_DROME	O46201	drosophila
526	2	5.1	31	1	ANP3_PAGBO	P02732	pagothernia
527	2	5.1	31	1	CEC1_PIG	P14661	sus scrofa
528	2	5.1	31	1	CIRB_CHAPA	P56879	chassalia p
529	2	5.1	31	1	COG5_BOVIN	P83437	bos taurus
530	2	5.1	31	1	COX4_NEUCR	P06809	neurospora

531	2	5.1	31	1	CTX2_CORVA	P82601	coremiocnem
532	2	5.1	31	1	CXD6_CONNI	P56710	conus nigro
533	2	5.1	31	1	CXG6_CONTE	P58922	conus texti
534	2	5.1	31	1	CXOA_CONPE	P56712	conus penna
535	2	5.1	31	1	CYLA_PSYLO	P56872	psychotria
536	2	5.1	31	1	CYO6_VIOOD	P58438	viola odora
537	2	5.1	31	1	DEF2_MESAU	P81466	mesocricetu
538	2	5.1	31	1	DEJP_DROME	P81160	drosophila
539	2	5.1	31	1	EFTU_STRLU	P52390	streptomyce
540	2	5.1	31	1	ENDB_CAMDR	P01203	camelus dro
541	2	5.1	31	1	ER29_BOVIN	P81623	bos taurus
542	2	5.1	31	1	ETFD_PARDE	P55932	paracoccus
543	2	5.1	31	1	FIBB_CANFA	P02677	canis famil
544	2	5.1	31	1	GP37_BPSP1	O48393	bacteriopha
545	2	5.1	31	1	GT_SERMA	P22416	serratia ma
546	2	5.1	31	1	GUN2_SCLSC	P21834	sclerotinia
547	2	5.1	31	1	H13_WHEAT	P15872	triticum ae
548	2	5.1	31	1	HEM2_PHAGO	P27687	phascolopsi
549	2	5.1	31	1	KLK1_CAVPO	P12322	cavia porce
550	2	5.1	31	1	LC70_LACPA	P80959	lactobacill
551	2	5.1	31	1	LCCB_LEUME	P81052	leuconostoc
552	2	5.1	31	1	LPRM_ECOLI	P10739	escherichia
553	2	5.1	31	1	MALK_PHOLU	P41124	photorhabdu
554	2	5.1	31	1	MDH_STRAR	P19982	streptomyce
555	2	5.1	31	1	NAP4_HUMAN	P19877	homo sapien
556	2	5.1	31	1	PETL_CHLVU	P56306	chlorella v
557	2	5.1	31	1	PETL_PORPU	P51221	porphyra pu
558	2	5.1	31	1	PRT3_CLUPA	P02337	clupea pall
559	2	5.1	31	1	PSAK_ANAVA	P23317	anabaena va
560	2	5.1	31	1	SC37_MESMA	P83407	mesobuthus
561	2	5.1	31	1	SCK5_ANDMA	P31719	androctonus
562	2	5.1	31	1	SCKL_LEIQH	P16341	leiurus qui
563	2	5.1	31	1	SODC_STRHE	P81163	striga herm
564	2	5.1	31	1	TX3_HETVE	P58427	heteropoda
565	2	5.1	31	1	Y603_ARCFU	O29652	archaeoglob
566	2	5.1	31	1	Y822_BORBU	O51762	borrelia bu
567	2	5.1	32	1	A2M_PACLE	P20738	pacifastacu
568	2	5.1	32	1	ATP0_PIG	P80021	sus scrofa
569	2	5.1	32	1	ATP7_SPIOL	P80088	spinacia ol
570	2	5.1	32	1	ATP0_SPIOL	P80087	spinacia ol
571	2	5.1	32	1	CAAP_MICEC	P21162	micromonosp
572	2	5.1	32	1	CAL0_BOVIN	P01260	bos taurus
573	2	5.1	32	1	CAL0_PIG	P01259	sus scrofa
574	2	5.1	32	1	CAR1_ECHCA	Q9prp9	echis carin
575	2	5.1	32	1	CEC_OIKKI	P83420	oiketicus k
576	2	5.1	32	1	COA1_BPIF1	O80295	bacteriopha
577	2	5.1	32	1	COA1_BPIKE	P03676	bacteriopha
578	2	5.1	32	1	COA2_BPFD	P03677	bacteriopha
579	2	5.1	32	1	COA2_BPIF1	O80296	bacteriopha
580	2	5.1	32	1	CRP_PLEPL	P12245	pleuronecte
581	2	5.1	32	1	CXG7_CONPE	P56711	conus penna
582	2	5.1	32	1	CY31_DESAC	P81078	desulfuromo
583	2	5.1	32	1	CYSB_FASHE	P80529	fasciola he
584	2	5.1	32	1	ER29_CHICK	P81628	gallus gall
585	2	5.1	32	1	ER29_TRIVU	P81629	trichosurus
586	2	5.1	32	1	ERH_PIG	P80230	sus scrofa
587	2	5.1	32	1	FF21_SALEN	P55224	salmonella

588	2	5.1	32	1	FLA1_METHU	P17603	methanospir
589	2	5.1	32	1	FRIH_ANAPL	P80145	anas platyr
590	2	5.1	32	1	GHR4_RAT	P33581	rattus norv
591	2	5.1	32	1	GLB4_LAMSP	P20413	lamellibrac
592	2	5.1	32	1	GT82_DICLA	P82608	dicentrarch
593	2	5.1	32	1	H2AZ_ONCMY	P22647	oncorhynchu
594	2	5.1	32	1	HCYC_CHEDE	P83172	cherax dest
595	2	5.1	32	1	IAPP_BOVIN	Q28207	bos taurus
596	2	5.1	32	1	IAPP_PIG	Q29119	sus scrofa
597	2	5.1	32	1	IAPP_SHEEP	Q28605	ovis aries
598	2	5.1	32	1	ILVB_ENTAE	Q09129	enterobacte
599	2	5.1	32	1	ITR2_CUCSA	P10291	cucumis sat
600	2	5.1	32	1	ITR3_CUCPE	P10293	cucurbita p
601	2	5.1	32	1	ITR4_CUCMA	P07853	cucurbita m
602	2	5.1	32	1	LEC_DOLAX	P02875	dolichos ax
603	2	5.1	32	1	MDH_NITAL	P10887	nitzschia a
604	2	5.1	32	1	MIFH_TRITR	P81748	trichuris t
605	2	5.1	32	1	NEUB_PIG	P01297	sus scrofa
606	2	5.1	32	1	OVOS_ANAPL	P20739	anas platyr
607	2	5.1	32	1	P1SM_LOXIN	P83045	loxosceles
608	2	5.1	32	1	PA22_AGKHP	P18997	agkistrodon
609	2	5.1	32	1	PA2_RHONO	P43318	rhopilema n
610	2	5.1	32	1	PETL_CHLRE	P50369	chlamydomon
611	2	5.1	32	1	PETM_GUITH	O78499	guillardia
612	2	5.1	32	1	PHNS_DESMU	P13062	desulfovibr
613	2	5.1	32	1	PHSS_DESBN	P13064	desulfovibr
614	2	5.1	32	1	PRT1_ESOLU	P02325	esox lucius
615	2	5.1	32	1	PRT1_ONCKE	P02327	oncorhynchu
616	2	5.1	32	1	PRT4_SCYCA	P30259	scyliorhinu
617	2	5.1	32	1	PRT5_ONCMY	P02334	oncorhynchu
618	2	5.1	32	1	PRT6_ONCMY	P08145	oncorhynchu
619	2	5.1	32	1	PRT9_ONCMY	P08147	oncorhynchu
620	2	5.1	32	1	PRTA_ONCMY	P12818	oncorhynchu
621	2	5.1	32	1	PRTE_HALME	P28308	halobacteri
622	2	5.1	32	1	PSBT_CYACA	O19927	cyanidium c
623	2	5.1	32	1	PSBT_GUITH	O78512	guillardia
624	2	5.1	32	1	PSBZ_EUGMY	Q8s191	euglena myx
625	2	5.1	32	1	RIP2_PHYDI	P34967	phytolacca
626	2	5.1	32	1	RK1_RABIT	P81655	oryctolagus
627	2	5.1	32	1	RS19_YEREN	Q56847	yersinia en
628	2	5.1	32	1	TAT_SIVM2	P05912	simian immu
629	2	5.1	32	1	TX29_PHONI	P29426	phoneutria
630	2	5.1	32	1	TXP7_APTSC	P49271	aptostichus
631	2	5.1	32	1	UC09_MAIZE	P80615	zea mays (m
632	2	5.1	32	1	Y169_TREPA	O83199	treponema p
633	2	5.1	32	1	YH17_HAEIN	P44295	haemophilus
634	2	5.1	32	1	YL55_CAEEL	P34435	caenorhabdi
635	2	5.1	32	1	YSCA_YEREN	Q01242	yersinia en
636	2	5.1	33	1	ACT_DICVI	Q24733	dictyocaulu
637	2	5.1	33	1	ATP7_SOLTU	P80496	solanum tub
638	2	5.1	33	1	BR2A_RANES	P40837	rana escule
639	2	5.1	33	1	BR2B_RANES	P40838	rana escule
640	2	5.1	33	1	BR2E_RANES	P32413	rana escule
641	2	5.1	33	1	BR2_RANBP	P32424	rana brevip
642	2	5.1	33	1	CECB_HELVI	P83414	heliobacter
643	2	5.1	33	1	CECC_HELVI	P83415	heliobacter
644	2	5.1	33	1	COA1_BPFD	P03675	bacterioph

645	2	5.1	33	1	COA2_BPI22	P15414	bacterioph
646	2	5.1	33	1	COA2_BPIKE	P03678	bacterioph
647	2	5.1	33	1	COXL_ONCMY	P80330	oncorhynch
648	2	5.1	33	1	CU89_HUMAN	P59042	homo sapien
649	2	5.1	33	1	CXO_CONVE	P83301	conus ventr
650	2	5.1	33	1	DBB2_DOLAU	P83376	dolabella a
651	2	5.1	33	1	DEF4_MESAU	P81468	mesocricetu
652	2	5.1	33	1	DHE3_PIG	P42174	sus scrofa
653	2	5.1	33	1	FABI_RHASA	P81175	rhamdia sap
654	2	5.1	33	1	GAST_CAVPO	P06885	cavia porce
655	2	5.1	33	1	GAST_CHIBR	P10034	chinchilla
656	2	5.1	33	1	GAST_DIDMA	P33713	didelphis m
657	2	5.1	33	1	GGN1_RANRU	P80395	rana rugosa
658	2	5.1	33	1	GGN2_RANRU	P80396	rana rugosa
659	2	5.1	33	1	GGN3_RANRU	P80397	rana rugosa
660	2	5.1	33	1	GLU2_ORENI	P81027	oreochromis
661	2	5.1	33	1	HF40_MAIZE	P82865	zea mays (m
662	2	5.1	33	1	HOXU_RHOOP	P22659	rhodococcus
663	2	5.1	33	1	LPPY_SALTY	P08522	salmonella
664	2	5.1	33	1	LPRH_ECOLI	P37324	escherichia
665	2	5.1	33	1	LYC2_HORSE	P81710	equus cabal
666	2	5.1	33	1	MHAA_STRCH	P80435	streptomyce
667	2	5.1	33	1	MYMY_MYTED	P81614	mytilus edu
668	2	5.1	33	1	OREX_BOVIN	P56717	bos taurus
669	2	5.1	33	1	OTCC_PSEPU	P11727	pseudomonas
670	2	5.1	33	1	PAP1_PARPV	P81865	pardachirus
671	2	5.1	33	1	PAP2_PARPV	P23067	pardachirus
672	2	5.1	33	1	PAP3_PARPV	P81866	pardachirus
673	2	5.1	33	1	PAP4_PARMA	P81861	pardachirus
674	2	5.1	33	1	PAP5_PARMA	P81862	pardachirus
675	2	5.1	33	1	PEN3_ADECU	P35987	canine aden
676	2	5.1	33	1	PETM_CYAPA	P48366	cyanophora
677	2	5.1	33	1	PK5_DICDI	P34104	dictyosteli
678	2	5.1	33	1	PRI1_ONCMY	P02326	oncorhynch
679	2	5.1	33	1	PRI2_ONCMY	P02328	oncorhynch
680	2	5.1	33	1	PSAI_SPIOL	P17228	spinacia ol
681	2	5.1	33	1	PSAK_CUCSA	P42051	cucumis sat
682	2	5.1	33	1	RL21_XENLA	P49628	xenopus lae
683	2	5.1	33	1	RL26_XENLA	P49629	xenopus lae
684	2	5.1	33	1	RL28_XENLA	P46780	xenopus lae
685	2	5.1	33	1	RRPO_BPBZ1	P09674	bacterioph
686	2	5.1	33	1	RS4_XENLA	P49401	xenopus lae
687	2	5.1	33	1	RT25_BOVIN	P82669	bos taurus
688	2	5.1	33	1	RUGA_RANRU	P80954	rana rugosa
689	2	5.1	33	1	RUGB_RANRU	P80955	rana rugosa
690	2	5.1	33	1	SC63_CANFA	P82008	canis famil
691	2	5.1	33	1	SCX9_BUTO	P04099	buthus occi
692	2	5.1	33	1	T1F_PARTE	Q27172	paramecium
693	2	5.1	33	1	TH10_CLOST	P81109	clostridium
694	2	5.1	33	1	TXH1_SELHU	P56676	selenocosmi
695	2	5.1	33	1	TXN3_SELHA	P83464	selenocosmi
696	2	5.1	33	1	VT1B_RAT	P58200	rattus norv
697	2	5.1	33	1	Y849_BORBU	O51789	borrelia bu
698	2	5.1	33	1	YC12_EUGGR	P31559	euglena gra
699	2	5.1	33	1	YC12_NEPOL	Q9tky6	nephroselmi
700	2	5.1	33	1	YC12_PINTH	P41600	pinus thunb
701	2	5.1	33	1	YL74_ARCFU	O28108	archaeoglob

702	2	5.1	33	1	YLCH_BP82	Q37869	bacterioph
703	2	5.1	33	1	YLCH_ECOLI	Q47268	escherichia
704	2	5.1	34	1	AMP2_CHICK	P80390	gallus gall
705	2	5.1	34	1	ASPG_PIG	P30918	sus scrofa
706	2	5.1	34	1	BR2C_RANES	P40839	rana escule
707	2	5.1	34	1	BUTH_ANDAU	P56685	androctonus
708	2	5.1	34	1	COXG_THUOB	P80976	thunnus obe
709	2	5.1	34	1	DEF7_RABIT	P80223	oryctolagus
710	2	5.1	34	1	ECAB_ECTTU	P49344	ectatomma t
711	2	5.1	34	1	EF2_RABIT	P55823	oryctolagus
712	2	5.1	34	1	EGGR_APLCA	P01363	aplysia cal
713	2	5.1	34	1	EM1_ENSMI	P27205	ensis minor
714	2	5.1	34	1	GAST_CAPHI	P04564	capra hircu
715	2	5.1	34	1	GUN1_SCLSC	P21833	sclerotinia
716	2	5.1	34	1	H1S_STRPU	P19376	strongyloce
717	2	5.1	34	1	HS7S_CUCMA	P31082	cucurbita m
718	2	5.1	34	1	ITR1_MOMCO	P82408	momordica c
719	2	5.1	34	1	ITR2_MOMCO	P82409	momordica c
720	2	5.1	34	1	LPTN_PROVU	P28779	proteus vul
721	2	5.1	34	1	M44E_HUMAN	Q96pg1	homo sapien
722	2	5.1	34	1	MYTA_MYTED	P81612	mytilus edu
723	2	5.1	34	1	PRT1_SAROR	P25327	sarda orien
724	2	5.1	34	1	PRT1_THUTH	P02321	thunnus thy
725	2	5.1	34	1	PRT2_THUTH	P02322	thunnus thy
726	2	5.1	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
727	2	5.1	34	1	PSAI_OENHO	Q9mtl2	oenothera h
728	2	5.1	34	1	PSAI_SOYBN	P49159	glycine max
729	2	5.1	34	1	PSBM_ARATH	P12169	arabidopsis
730	2	5.1	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
731	2	5.1	34	1	PSBM_CHLRE	P92277	chlamydomon
732	2	5.1	34	1	PSBM_MAIZE	P48189	zea mays (m
733	2	5.1	34	1	PSBM_MARPO	P12168	marchantia
734	2	5.1	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
735	2	5.1	34	1	PSBM_OENHO	Q9mtm8	oenothera h
736	2	5.1	34	1	PSBM_PEA	P34833	pisum sativ
737	2	5.1	34	1	PSBM_PSINU	Q8wi22	psilotum nu
738	2	5.1	34	1	PSBM_WHEAT	Q9xps6	triticum ae
739	2	5.1	34	1	PTU1_PEITU	P58606	peirates tu
740	2	5.1	34	1	PYSB_METBA	P80522	methanosarc
741	2	5.1	34	1	RNL1_PIG	P15466	sus scrofa
742	2	5.1	34	1	SCXM_SCOMA	P80719	scorpio mau
743	2	5.1	34	1	THEM_MALSU	P13858	malbranchea
744	2	5.1	34	1	TX1_SCOGR	P56855	scodra gris
745	2	5.1	34	1	TXP5_BRASM	P49266	brachypelma
746	2	5.1	34	1	Y05J_BPT4	P39239	bacterioph
747	2	5.1	34	1	Y224_TREPA	O83253	treponema p
748	2	5.1	34	1	Y848_BORBU	O51788	borrelia bu
749	2	5.1	34	1	Y967_HAEIN	P44086	haemophilus
750	2	5.1	34	1	YC12_PORPU	P51385	porphyra pu
751	2	5.1	34	1	YMIA_AGR TU	P38437	agrobacteri
752	2	5.1	35	1	C550_BACHA	P80091	bacillus ha
753	2	5.1	35	1	CEC4_BOMMO	P14666	bombyx mori
754	2	5.1	35	1	CECA_AEDAL	P81417	aedes albop
755	2	5.1	35	1	CECA_HELVI	P83413	heliothis v
756	2	5.1	35	1	CECB_ANTPE	P01509	antheraea p
757	2	5.1	35	1	CHI1_CASSA	P29137	castanea sa
758	2	5.1	35	1	COPA_CANFA	P40765	canis famil

759	2	5.1	35	1	CPI2_PIG	P80736	sus scrofa
760	2	5.1	35	1	DEFB_MYTED	P81611	mytilus edu
761	2	5.1	35	1	END4_YEREN	P42691	yersinia en
762	2	5.1	35	1	FAS_CAPHI	P08757	capra hircu
763	2	5.1	35	1	FLAV_NOSSM	P35707	nostoc sp.
764	2	5.1	35	1	GBGU_MOUSE	Q61017	mus musculu
765	2	5.1	35	1	GP58_BPSP1	O48412	bacterioph
766	2	5.1	35	1	GRDB_CLOPU	P55793	clostridium
767	2	5.1	35	1	GUR_GYMSY	P25810	gymnema syl
768	2	5.1	35	1	HCYA_CHEDE	P83173	cherax dest
769	2	5.1	35	1	HMWC_DESGI	P38588	desulfovibr
770	2	5.1	35	1	IAAC_HORVU	P34951	hordeum vul
771	2	5.1	35	1	KPPR_PINPS	P81664	pinus pinas
772	2	5.1	35	1	LCGB_LACLA	P36962	lactococcus
773	2	5.1	35	1	LEC1_CYTSE	P22970	cytissus ses
774	2	5.1	35	1	LEC3_ULEEU	P23032	ulex europe
775	2	5.1	35	1	PBP1_LYMDI	P34176	lymantria d
776	2	5.1	35	1	PBP_HYACE	P34175	hyalophora
777	2	5.1	35	1	PBP_ORGPS	P34178	orgyia pseu
778	2	5.1	35	1	PHI1_MYTCA	P35422	mytilus cal
779	2	5.1	35	1	PSAI_CYAPA	P48116	cyanophora
780	2	5.1	35	1	PSBM_SYNY3	P72701	synechocyst
781	2	5.1	35	1	SCKG_PANIM	Q10726	pandinus im
782	2	5.1	35	1	SCKK_TITSE	P56219	tityus serr
783	2	5.1	35	1	SCX1_BUTSI	P15229	buthus sind
784	2	5.1	35	1	SPRC_PIG	P20112	sus scrofa
785	2	5.1	35	1	THPA_THADA	P21381	thamatococ
786	2	5.1	35	1	TMTX_MESTA	Q9bn12	mesobuthus
787	2	5.1	35	1	TX1_GRASP	P56852	grammostola
788	2	5.1	35	1	TX2_GRASP	P56853	grammostola
789	2	5.1	35	1	TXAG_AGEOP	P31328	agelena opu
790	2	5.1	35	1	TXH4_SELHU	P83303	selenocosmi
791	2	5.1	35	1	TXKS_STOHE	P29187	stoichactis
792	2	5.1	35	1	TXN4_SELHA	P83471	selenocosmi
793	2	5.1	35	1	VL3_PAPVD	P06919	deer papill
794	2	5.1	35	1	VSPA_CERVI	P18692	cerastes vi
795	2	5.1	35	1	Y210_HAEIN	P43964	haemophilus
796	2	5.1	35	1	Y320_BORBU	O51299	borrelia bu
797	2	5.1	35	1	Y644_ARCFU	O29613	archaeoglob
798	2	5.1	35	1	Y845_BORBU	O51785	borrelia bu
799	2	5.1	35	1	Y847_BORBU	O51787	borrelia bu
800	2	5.1	35	1	YC69_ARCFU	O28999	archaeoglob
801	2	5.1	36	1	ANFV_ANGJA	P22642	anguilla ja
802	2	5.1	36	1	C3L1_BOVIN	P30922	bos taurus
803	2	5.1	36	1	CBBA_NITVU	P37102	nitrobacter
804	2	5.1	36	1	CYC7_GEOME	P81894	geobacter m
805	2	5.1	36	1	DESR_DESGI	P00273	desulfovibr
806	2	5.1	36	1	F4RE_METOG	P80951	methanogeni
807	2	5.1	36	1	GLU1_ORENI	P81026	oreochromis
808	2	5.1	36	1	GLUC_HYDCO	P09682	hydrolagus
809	2	5.1	36	1	H1L5_ENSMI	P27203	ensis minor
810	2	5.1	36	1	IAA_STRAU	P04082	streptomyce
811	2	5.1	36	1	IOB1_ISYOB	P58609	isyndus obs
812	2	5.1	36	1	KAD_STRGR	P53398	streptomyce
813	2	5.1	36	1	LHG_RHOVI	P04126	rhodopseudo
814	2	5.1	36	1	MFA1_YEAST	P34165	saccharomyc
815	2	5.1	36	1	NLTP_PINPI	P26912	pinus pinea

816	2	5.1	36	1	OST2_CHICK	P80897	gallus gall
817	2	5.1	36	1	PAHO_ALLMI	P06305	alligator m
818	2	5.1	36	1	PAHO_CERSI	P37999	ceratotheri
819	2	5.1	36	1	PAHO_CHIBR	P41519	chinchilla
820	2	5.1	36	1	PAHO_EQUZE	P38000	equus zebra
821	2	5.1	36	1	PAHO_ERIEU	P41335	erinaceus e
822	2	5.1	36	1	PAHO_MACMU	P33684	macaca mula
823	2	5.1	36	1	PAHO_RANCA	P15427	rana catesb
824	2	5.1	36	1	PAHO_RANTE	P31229	rana tempor
825	2	5.1	36	1	PAHO_TAPPI	P39659	tapirus pin
826	2	5.1	36	1	PETM_SYNY3	P74810	synechocyst
827	2	5.1	36	1	PGKH_CHLFU	P36232	chlorella f
828	2	5.1	36	1	PMY_PETMA	P80024	petromyzon
829	2	5.1	36	1	PSAI_ANGLY	P28251	angiopteris
830	2	5.1	36	1	PSAI_BRAOL	Q31909	brassica ol
831	2	5.1	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
832	2	5.1	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
833	2	5.1	36	1	PSAI_CHLVU	P58214	chlorella v
834	2	5.1	36	1	PSAI_CYACA	Q9tm24	cyanidium c
835	2	5.1	36	1	PSAI_GUITH	O78462	guillardia
836	2	5.1	36	1	PSAI_HORVU	P13165	hordeum vul
837	2	5.1	36	1	PSAI_MAIZE	P30980	zea mays (m
838	2	5.1	36	1	PSAI_MARPO	P12185	marchantia
839	2	5.1	36	1	PSAI_MESVI	Q9muq4	mesostigma
840	2	5.1	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
841	2	5.1	36	1	PSAI_ORYSA	P12186	oryza sativ
842	2	5.1	36	1	PSAI_PICAB	O47040	picea abies
843	2	5.1	36	1	PSAI_PORPU	P51387	porphyra pu
844	2	5.1	36	1	PSAI_PSINU	Q8wi10	psilotum nu
845	2	5.1	36	1	PSAI_TOBAC	P12187	nicotiana t
846	2	5.1	36	1	PSAI_WHEAT	P25410	triticum ae
847	2	5.1	36	1	PSBI_ARATH	P09970	arabidopsis
848	2	5.1	36	1	PSBI_HORVU	P25876	hordeum vul
849	2	5.1	36	1	PSBI_MARPO	P09969	marchantia
850	2	5.1	36	1	PSBI_ORYSA	P12161	oryza sativ
851	2	5.1	36	1	PSBI_PINTH	P41599	pinus thunb
852	2	5.1	36	1	PSBI_PSEMZ	P29796	pseudotsuga
853	2	5.1	36	1	PSBM_CHLVU	P56325	chlorella v
854	2	5.1	36	1	PSBM_SYNEL	Q8dha7	synechococc
855	2	5.1	36	1	PYY_MYOSC	P09641	myoxocephal
856	2	5.1	36	1	PYY_ORENI	P81028	oreochromis
857	2	5.1	36	1	PYY_PIG	P01305	sus scrofa
858	2	5.1	36	1	PYY_RANRI	P29204	rana ridibu
859	2	5.1	36	1	RET4_CHICK	P30370	gallus gall
860	2	5.1	36	1	RL6_HALCU	P05968	halobacteri
861	2	5.1	36	1	SCK2_CENLL	P45630	centruroide
862	2	5.1	36	1	SCX1_BUTEU	P15220	buthus eupe
863	2	5.1	36	1	SCX8_BUTOC	P04098	buthus occi
864	2	5.1	36	1	SCXL_LEIQU	P45639	leiurus qui
865	2	5.1	36	1	SPYY_PHYBI	P80952	phyllomedus
866	2	5.1	36	1	TERN_PSEUS	P82321	pseudacanth
867	2	5.1	36	1	TLN1_CHICK	P54939	gallus gall
868	2	5.1	36	1	TX1B_AGEAP	P15970	agelenopsis
869	2	5.1	36	1	TX35_PHONI	P81791	phoneutria
870	2	5.1	36	1	TXAM_METSE	P11495	metridium s
871	2	5.1	36	1	TXD3_PARLU	P83258	paracoelote
872	2	5.1	36	1	TXJA_HADVE	P82227	hadronyche

873	2	5.1	36	1	TXJB_HADVE	P82226	hadronyche
874	2	5.1	36	1	Y16L_BPT4	P39244	bacterioph
875	2	5.1	36	1	Y260_BACHD	Q9kg53	bacillus ha
876	2	5.1	36	1	Y4KD_BPCHP	P19188	bacterioph
877	2	5.1	36	1	Y609_ARCFU	O29646	archaeoglob
878	2	5.1	36	1	Y609_BORBU	O51554	borrelia bu
879	2	5.1	36	1	Y619_ARCFU	O29636	archaeoglob
880	2	5.1	36	1	YG50_HAEIN	P44281	haemophilus
881	2	5.1	36	1	YRKG_BACSU	P54434	bacillus su
882	2	5.1	37	1	AFP4_MALPA	P83138	malva parvi
883	2	5.1	37	1	ATPO_SOLTU	P80504	solanum tub
884	2	5.1	37	1	B2MG_ORENI	Q03423	oreochromis
885	2	5.1	37	1	CAL1_PIG	P30880	sus scrofa
886	2	5.1	37	1	CAL1_SHEEP	P30881	ovis aries
887	2	5.1	37	1	CG2S_LUPAN	P09930	lupinus ang
888	2	5.1	37	1	CS40_STAAU	P81684	staphylococ
889	2	5.1	37	1	CUP4_SARBU	P14486	sarcophaga
890	2	5.1	37	1	DEF4_ANDAU	P56686	androctonus
891	2	5.1	37	1	DEFA_MYTED	P81610	mytilus edu
892	2	5.1	37	1	ECAA_ECTTU	P49343	ectatomma t
893	2	5.1	37	1	ES2A_RANES	P40845	rana escule
894	2	5.1	37	1	ES2B_RANES	P40846	rana escule
895	2	5.1	37	1	F13A_BOVIN	P12260	bos taurus
896	2	5.1	37	1	IAPP_CRIGR	P19890	cricetulus
897	2	5.1	37	1	LCNM_LACLA	P83002	lactococcus
898	2	5.1	37	1	LPPY_SERMA	P19937	serratia ma
899	2	5.1	37	1	MAUR_PARVE	Q56462	paracoccus
900	2	5.1	37	1	ME22_EUPRA	P58548	euplotes ra
901	2	5.1	37	1	MIBP_PSESP	P04576	pseudomonas
902	2	5.1	37	1	NLT3_VITSX	P80273	vitis sp. (
903	2	5.1	37	1	NLT4_VITSX	P80274	vitis sp. (
904	2	5.1	37	1	NUFM_SOLTU	P80266	solanum tub
905	2	5.1	37	1	OP2A_OXYKI	P83248	oxyopes kit
906	2	5.1	37	1	OP2B_OXYKI	P83249	oxyopes kit
907	2	5.1	37	1	OP2C_OXYKI	P83250	oxyopes kit
908	2	5.1	37	1	OP2D_OXYKI	P83251	oxyopes kit
909	2	5.1	37	1	PETG_ANASP	P58246	anabaena sp
910	2	5.1	37	1	PETG_ANAVA	Q913p7	anabaena va
911	2	5.1	37	1	PETG_ARATH	P56775	arabidopsis
912	2	5.1	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
913	2	5.1	37	1	PETG_CHLEU	P46304	chlamydomon
914	2	5.1	37	1	PETG_CHLRE	Q08362	chlamydomon
915	2	5.1	37	1	PETG_CHLVU	P56305	chlorella v
916	2	5.1	37	1	PETG_CUSRE	P30398	cuscuta ref
917	2	5.1	37	1	PETG_CYAPA	P14236	cyanophora
918	2	5.1	37	1	PETG_EUGGR	P30396	euglena gra
919	2	5.1	37	1	PETG_GUIITH	O78505	guillardia
920	2	5.1	37	1	PETG_MARPO	P12120	marchantia
921	2	5.1	37	1	PETG_MESVI	Q9mun3	mesostigma
922	2	5.1	37	1	PETG_NEPOL	Q9tky8	nephroselmi
923	2	5.1	37	1	PETG_ODOSI	P49470	odontella s
924	2	5.1	37	1	PETG_ORYSA	P12121	oryza sativ
925	2	5.1	37	1	PETG_PINTH	P41614	pinus thunb
926	2	5.1	37	1	PETG_PSINU	Q8wi02	psilotum nu
927	2	5.1	37	1	PETG_SYNEL	Q8dk12	synechococc
928	2	5.1	37	1	PETG_SYNP7	Q9z3g1	synechococc
929	2	5.1	37	1	PIIL_ACHLY	P81720	achromobact

930	2	5.1	37	1	POLN_WEEV	P13896	western equ
931	2	5.1	37	1	PRF1_RAT	P18889	rattus norv
932	2	5.1	37	1	PRT3_SCYCA	P30258	scyliorhinu
933	2	5.1	37	1	PSAI_ARATH	P56768	arabidopsis
934	2	5.1	37	1	PSAJ_EUGGR	P30394	euglena gra
935	2	5.1	37	1	PSBL_ARATH	P29301	arabidopsis
936	2	5.1	37	1	PSBL_ORYSA	P12166	oryza sativ
937	2	5.1	37	1	PSBM_PINTH	P41608	pinus thunb
938	2	5.1	37	1	PSBY_CYACA	O19893	cyanidium c
939	2	5.1	37	1	RK36_ARATH	P12144	arabidopsis
940	2	5.1	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
941	2	5.1	37	1	RK36_CHLVU	P56360	chlorella v
942	2	5.1	37	1	RK36_CYACA	Q9tlu9	cyanidium c
943	2	5.1	37	1	RK36_CYAPA	P48131	cyanophora
944	2	5.1	37	1	RK36_EPIVI	P30069	epifagus vi
945	2	5.1	37	1	RK36_LOTJA	Q9bbq2	lotus japon
946	2	5.1	37	1	RK36_MARPO	P12142	marchantia
947	2	5.1	37	1	RK36_ODOSI	P49568	odontella s
948	2	5.1	37	1	RK36_OENHO	Q9mtj1	oenothera h
949	2	5.1	37	1	RK36_ORYSA	P12143	oryza sativ
950	2	5.1	37	1	RK36_PINTH	P41631	pinus thunb
951	2	5.1	37	1	RK36_PSINU	Q8why9	psilotum nu
952	2	5.1	37	1	RK36_SPIOL	P12230	spinacia ol
953	2	5.1	37	1	RL36_ANASP	Q8ypk0	anabaena sp
954	2	5.1	37	1	RL36_AQUAE	O66487	aquifex aeo
955	2	5.1	37	1	RL36_BACHD	O50631	bacillus ha
956	2	5.1	37	1	RL36_BACST	P07841	bacillus st
957	2	5.1	37	1	RL36_BACSU	P20278	bacillus su
958	2	5.1	37	1	RL36_BORBU	O51452	borrelia bu
959	2	5.1	37	1	RL36_CAMJE	Q9pm84	campylobact
960	2	5.1	37	1	RL36_CLOAB	Q97ek2	clostridium
961	2	5.1	37	1	RL36_CLOPE	Q8xhu7	clostridium
962	2	5.1	37	1	RL36_HAEIN	P46361	haemophilus
963	2	5.1	37	1	RL36_HELPJ	Q9zjt1	helicobacte
964	2	5.1	37	1	RL36_HELPY	P56058	helicobacte
965	2	5.1	37	1	RL36_LEPIN	Q9xd13	leptospira
966	2	5.1	37	1	RL36_LISMO	Q927n0	listeria mo
967	2	5.1	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
968	2	5.1	37	1	RL36_MYCGE	P47420	mycoplasma
969	2	5.1	37	1	RL36_MYCPN	P52864	mycoplasma
970	2	5.1	37	1	RL36_MYCPU	Q98q05	mycoplasma
971	2	5.1	37	1	RL36_MYCSP	P38015	mycoplasma
972	2	5.1	37	1	RL36_NEIMA	Q9jrb2	neisseria m
973	2	5.1	37	1	RL36_PASMU	P57942	pasteurella
974	2	5.1	37	1	RL36_STAAM	Q99s42	staphylococ
975	2	5.1	37	1	RL36_SYNP6	O24707	synechococc
976	2	5.1	37	1	RL36_THETN	Q8r7x8	thermoanaer
977	2	5.1	37	1	RL36_TREPA	O83239	treponema p
978	2	5.1	37	1	RL36_UREPA	Q9pqn7	ureaplasma
979	2	5.1	37	1	RL36_VIBCH	P78001	vibrio chol
980	2	5.1	37	1	RL7_CLOPA	P05393	clostridium
981	2	5.1	37	1	RS15_HELLU	P52820	helix lucor
982	2	5.1	37	1	RUGC_RANRU	P80956	rana rugosa
983	2	5.1	37	1	SCK2_LEIQH	P45628	leiurus qui
984	2	5.1	37	1	SCK3_BUTOC	P59290	buthus occi
985	2	5.1	37	1	SCK3_PARTR	P83112	parabuthus
986	2	5.1	37	1	SCKA_TITSE	P46114	tityus serr

987	2	5.1	37	1	SCKC_LEIQH	P13487 leiurus qui
988	2	5.1	37	1	TX3D_AGEAP	P81746 agelenopsis
989	2	5.1	37	1	TXD1_PARLU	P83256 paracoelote
990	2	5.1	37	1	TXD2_PARLU	P83257 paracoelote
991	2	5.1	37	1	TXD4_PARLU	P83259 paracoelote
992	2	5.1	37	1	TXJC_HADVE	P82228 hadronyche
993	2	5.1	37	1	TXKB_BUNGR	P29186 bunodosoma
994	2	5.1	37	1	TXM2_AGEAP	P11058 agelenopsis
995	2	5.1	37	1	TXM4_AGEAP	P11060 agelenopsis
996	2	5.1	37	1	TXM5_AGEAP	P11061 agelenopsis
997	2	5.1	37	1	TXM6_AGEAP	P11062 agelenopsis
998	2	5.1	37	1	TXOF_HADVE	P81599 hadronyche
999	2	5.1	37	1	TXP3_APTSC	P49268 aptostichus
1000	2	5.1	37	1	VA1_BPBF2	P19347 bacterioph

ALIGNMENTS

RESULT 1

PETL_ARATH

ID PETL_ARATH STANDARD; PRT; 31 AA.

AC P56776;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit petL).

GN PETL OR ATCG00590.

OS Arabidopsis thaliana (Mouse-ear cress).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20039611; PubMed=10574454;

RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;

RT "Complete structure of the chloroplast genome of Arabidopsis thaliana.";

RL DNA Res. 6:283-290(1999).

CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR

CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND

CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL

CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON

CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.

CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.

CC -!- SIMILARITY: Belongs to the petL family.

CC -----

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DR EMBL; AP000423; BAA84403.1; -.

DR HAMAP; MF_00433; -, 1.

DR Pfam; PF05115; PetL; 1.

KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;

KW Thylakoid.

FT TRANSMEM 4 24 POTENTIAL.

SQ SEQUENCE 31 AA; 3401 MW; BEE4295D2F2B854F CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20

|||||

Db 11 LLAAL 15

RESULT 2

PETL_BETVU

ID PETL_BETVU STANDARD; PRT; 31 AA.

AC P46612;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).

GN PETL.

OS Beta vulgaris (Sugar beet).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

OX NCBI_TaxID=161934;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Altissima; TISSUE=Leaf;

RA Ran Z., Michaelis G.;

RT "Mapping of a chloroplast RFLP marker associated with the CMS

RT cytoplasm of sugar beet (Beta vulgaris).";

RL Theor. Appl. Genet. 91:836-840(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. TK81-O; TISSUE=Leaf;

RX MEDLINE=95254673; PubMed=7736615;

RA Kubo T., Yanai Y., Kinoshita T., Mikami T.;

RT "The chloroplast trnP-trnW-petG gene cluster in the mitochondrial

RT genomes of Beta vulgaris, B. trigyna and B. webbiana: evolutionary

RT aspects.";

RL Curr. Genet. 27:285-289(1995).

CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR

CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND

CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL

CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON

CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.

CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.

CC -- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; X87637; CAA60970.1; -.
 DR EMBL; D38019; BAA07217.1; -.
 DR EMBL; X87636; CAA60965.1; -.
 DR PIR; T14568; T14568.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3400 MW; BEE4294AF46F754F CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 3

PETL_MAIZE

ID PETL_MAIZE STANDARD; PRT; 31 AA.
 AC P19445;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Zea mays (Maize).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haley J., Bogorad L.;
 RL Submitted (MAY-1989) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95395841; PubMed=7666415;
 RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
 RT "Complete sequence of the maize chloroplast genome: gene content,
 RT hotspots of divergence and fine tuning of genetic information by
 RT transcript editing.";

RL J. Mol. Biol. 251:614-628(1995).

CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.

CC -----
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 CC -----

DR EMBL; J04502; AAA84479.1; -.
 DR EMBL; X86563; CAA60303.1; -.
 DR PIR; S58569; S58569.
 DR MaizeDB; 69195; -.
 DR HAMAP; MF_00433; -, 1.
 DR Pfam; PF05115; PetL; 1.

KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.

FT TRANSMEM 4 24 POTENTIAL.

SQ SEQUENCE 31 AA; 3456 MW; 0AE4294FA7E8B48E CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 4

PETL_OENHO

ID PETL_OENHO STANDARD; PRT; 31 AA.
 AC Q9MTK4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Oenothera hookeri (Hooker's evening primrose).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Onagraceae; Oenothera.
 OX NCBI_TaxID=85636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Johansen;
 RX MEDLINE=20309318; PubMed=10852478;

RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
 RA Chiu W.-L., Sears B.;
 RT "Complete nucleotide sequence of the *Oenothera elata* plastid
 RT chromosome, representing plastome I of the five distinguishable
 RT *Eucenothera* plastomes.";
 RL Mol. Gen. Genet. 263:581-585(2000).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; AJ271079; CAB67175.1; -.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3415 MW; A015C65D2F325493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 5

PETL_ORYSA

ID PETL_ORYSA STANDARD; PRT; 31 AA.
 AC P12180;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS *Oryza sativa* (Rice).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; *Oryza*.
 OX NCBI_TaxID=4530;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RX MEDLINE=89364698; PubMed=2770692;
 RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
 RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
 RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.;
 RT "The complete sequence of the rice (*Oryza sativa*) chloroplast genome:
 RT intermolecular recombination between distinct tRNA genes accounts for
 RT a major plastid DNA inversion during the evolution of the cereals.";
 RL Mol. Gen. Genet. 217:185-194(1989).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; X15901; CAA33966.1; -.
 DR PIR; S05124; S05124.
 DR Gramene; P12180; -.
 DR HAMAP; MF_00433; -, 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3442 MW; BEE4294FBC84B0C2 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 6

PETL_PSINU

ID PETL_PSINU STANDARD; PRT; 31 AA.
 AC Q8WI03;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Psilotum nudum (Whisk fern).

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Psilotophyta; Psilotales; Psilotaceae; Psilotum.
 OX NCBI_TaxID=3240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kingyoku;
 RA Wakasugi T., Nishikawa A., Yamada K., Sugiura M.;
 RT "Complete nucleotide sequence of the chloroplast genome from a fern,
 RT Psilotum nudum."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: The cytochrome b6-f complex functions in the linear
 CC cross-membrane transport of electrons between photosystem II and
 CC I, as well as in cyclic electron flow around photosystem I. PetL
 CC is important for photoautotrophic growth as well as for electron
 CC transfer efficiency and stability of the cytochrome b6-f complex.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; AP004638; BAB84234.1; -.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Respiratory chain; Transmembrane; Thylakoid;
 KW Chloroplast.
 SQ SEQUENCE 31 AA; 3392 MW; 84D427FB6FDCC51B CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 7

PETL_SPIOL

ID PETL_SPIOL STANDARD; PRT; 31 AA.
 AC Q9M3L0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Geant d'hiver, and cv. Monatol;
 RX MEDLINE=21187424; PubMed=11292076;
 RA Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
 RA Herrmann R.G., Mache R.;
 RT "The plastid chromosome of spinach (*Spinacia oleracea*): complete
 RT nucleotide sequence and gene organization."
 RL Plant Mol. Biol. 45:307-315(2001).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; AJ400848; CAB88746.1; -.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3390 MW; BEE4294AF46C457C CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 8

PETL_TOBAC

ID PETL_TOBAC STANDARD; PRT; 31 AA.
 AC P12181;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.

OS Nicotiana tabacum (Common tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bright Yellow 4;
 RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
 RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
 RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,
 RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
 RA Tohdoh N., Shimada H., Sugiura M.;
 RT "The complete nucleotide sequence of the tobacco chloroplast genome:
 RT its gene organization and expression."
 RL EMBO J. 5:2043-2049(1986).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; Z00044; CAA77419.1; -.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3389 MW; BEE4294FA4364493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

RESULT 9

PETL_WHEAT

ID PETL_WHEAT STANDARD; PRT; 31 AA.
 AC P58247;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Triticum aestivum (Wheat).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT complete sequence and contig clones.";
RL Plant Mol. Biol. Rep. 18:243-253(2000).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
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CC -----
DR EMBL; AB042240; BAB47051.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3426 MW; BEE4294AF7BDB493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 11 LLAAL 15

RESULT 10
REV_SIVM2
ID REV_SIVM2 STANDARD; PRT; 37 AA.

AC P08809;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE REV protein (Anti-repression transactivator protein) (ART/TRS)
 DE (Fragment).
 GN REV.
 OS Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11734;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122665; PubMed=2893293;
 RA Kestler H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
 RA King N.W., Daniel M.D., Desrosiers R.C.;
 RT "Comparison of simian immunodeficiency virus isolates.";
 RL Nature 331:619-622(1988).
 CC -!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
 CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
 CC -!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
 CC -!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
 CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
 CC -!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
 CC -----
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 CC -----
 DR EMBL; X06879; -; NOT_ANNOTATED_CDS.
 DR HIV; X06879; REV\$MM251.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00424; REV; 1.
 KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 4633 MW; 059C315CC56C5583 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALAD 6
 |||||
 Db 28 LALAD 32

RESULT 11
 PA22_MICNI
 ID PA22_MICNI STANDARD; PRT; 28 AA.
 AC P21791;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phospholipase A2 isozyme 2 (EC 3.1.1.4) (Phosphatidylcholine
 DE 2-acylhydrolase) (Fragment).
 OS *Micrurus nigrocinctus* (Central American coral snake) (Gargantilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; *Micrurus*.
 OX NCBI_TaxID=8635;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Mochca-Morales J., Martin B.M., Zamudio F.Z., Possani L.D.;
 RT "Isolation and characterization of three toxic phospholipases from
 RT the venom of the coral snake *Micrurus nigrocinctus*.";
 RL Toxicon 28:616-617(1990).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular
 CC transmission by blocking acetylcholine release from the nerve
 CC termini. Acts presynaptically.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
 CC SUBFAMILY.
 DR PIR; B35948; B35948.
 DR HSSP; P15445; 1A3D.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
 KW Presynaptic neurotoxin; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3373 MW; 6979B52DF2D718BC CRC64;

Query Match 10.3%; Score 4; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 RHWL 26
 ||||
 Db 15 RHWL 18

RESULT 12

PETL_CYAPA

ID PETL_CYAPA STANDARD; PRT; 28 AA.
 AC P48102;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS *Cyanophora paradoxa*.
 OG Cyanelle.

OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
 OX NCBI_TaxID=2762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX LB 555 / Pringsheim;
 RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
 RA Bryant D.A.;
 RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
 RL Plant Mol. Biol. Rep. 13:327-332(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX LB 555 / Pringsheim;
 RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
 RA Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
 RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
 RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:
 RT the genetic complexity of a primitive plastid.";
 RL (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
 RL Schwemmler W. (eds.);
 RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
 RL (1997).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; U30821; AAA81268.1; -.
 DR PIR; T06925; T06925.
 DR HAMAP; MF_00433; -; 1.
 KW Electron transport; Cyanelle; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 2 22 POTENTIAL.
 SQ SEQUENCE 28 AA; 3106 MW; ADAE8353D596AF3C CRC64;

Query Match 10.3%; Score 4; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
 ||||
 Db 14 LALA 17

RESULT 13
 PETN_GUITH
 ID PETN_GUITH STANDARD; PRT; 29 AA.

AC O78498;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
 DE petN).
 GN PETN OR YCF6.
 OS Guillardia theta (Cryptomonas phi).
 OG Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=55529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99128221; PubMed=9929392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Guillardia theta:
 RT complete sequence and conserved syntenic groups confirm its common
 RT ancestry with red algae."
 RL J. Mol. Evol. 48:236-244(1999).
 CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
 CC AND/OR STABILITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petN family.
 CC -----
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 CC -----
 DR EMBL; AF041468; AAC35689.1; -.
 DR HAMAP; MF_00395; -; 1.
 DR InterPro; IPR005497; PetN.
 DR Pfam; PF03742; PetN; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.
 FT TRANSMEM 3 23 POTENTIAL.
 SQ SEQUENCE 29 AA; 3231 MW; 13FB2B1B7B3525BD CRC64;

Query Match 10.3%; Score 4; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
 ||||
 Db 18 SLAL 21

RESULT 14
 PETN_ODOSI
 ID PETN_ODOSI STANDARD; PRT; 29 AA.
 AC P49527;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
 DE petN).
 GN PETN OR YCF6.
 OS Odontella sinensis (Marine centric diatom).
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
 OX NCBI_TaxID=2839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 RT Odontella sinensis."
 RL Plant Mol. Biol. Rep. 13:336-342(1995).
 CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
 CC AND/OR STABILITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petN family.
 CC -----
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 CC -----
 DR EMBL; Z67753; CAA91699.1; -.
 DR PIR; S78326; S78326.
 DR HAMAP; MF_00395; -; 1.
 DR InterPro; IPR005497; PetN.
 DR Pfam; PF03742; PetN; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.
 FT TRANSMEM 3 23 POTENTIAL.
 SQ SEQUENCE 29 AA; 3249 MW; E1589B4ABBB4C5A0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLAL 4
 ||||
 Db 18 SLAL 21

RESULT 15

PETN_SKECO

ID PETN_SKECO STANDARD; PRT; 29 AA.

AC 096807;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit

DE petN).

GN YCF6.
 OS Skeletonema costatum (Marine centric diatom).
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Thalassiosirophycidae; Thalassiosirales; Skeletonemataceae;
 OC Skeletonema.
 OX NCBI_TaxID=2843;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIES-323;
 RA Tada N., Otsuka S., Oyaizu H., Matsumoto S.;
 RT "Plastid DNA sequences of Skeletonema costatum NIES 323."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
 CC AND/OR STABILITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petN family.
 CC -----
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 CC -----
 DR EMBL; AJ132265; CAA10628.1; -.
 DR HAMAP; MF_00395; -; 1.
 DR InterPro; IPR005497; PetN.
 DR Pfam; PF03742; PetN; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.
 FT TRANSMEM 3 23 POTENTIAL.
 SQ SEQUENCE 29 AA; 3221 MW; E1588B90DE14C5A0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLAL 4
 ||||
 Db 18 SLAL 21

RESULT 16
 PETN_CYACA
 ID PETN_CYACA STANDARD; PRT; 31 AA.
 AC Q9TLR6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
 DE petN).
 GN PETN OR YCF42.
 OS Cyanidium caldarium.
 OG Chloroplast.

OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
 OC Cyanidium.
 OX NCBI_TaxID=2771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RK-1;
 RX MEDLINE=20496959; PubMed=11040290;
 RA Gloeckner G., Rosenthal A., Valentin K.-U.;
 RT "The structure and gene repertoire of an ancient red algal plastid
 RT genome.";
 RL J. Mol. Evol. 51:382-390(2000).
 CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
 CC AND/OR STABILITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petN family.
 CC -----
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 CC -----
 DR EMBL; AF022186; AAF12891.1; -.
 DR HAMAP; MF_00395; -; 1.
 DR InterPro; IPR005497; PetN.
 DR Pfam; PF03742; PetN; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.
 FT TRANSMEM 5 25 POTENTIAL.
 SQ SEQUENCE 31 AA; 3458 MW; 79D1E8E4E2493319 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
 ||||
 Db 20 SLAL 23

RESULT 17

PSAM_CHLVU

ID PSAM_CHLVU STANDARD; PRT; 31 AA.
 AC P56314;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM.
 OS Chlorella vulgaris.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 OC Chlorellaceae; Chlorella.
 OX NCBI_TaxID=3077;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IAM C-27 / Tamiya;
 RX MEDLINE=97303241; PubMed=9159184;
 RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
 RA Inamura A., Yoshinaga K., Sugiura M.;
 RT "Complete nucleotide sequence of the chloroplast genome from the
 RT green alga *Chlorella vulgaris*: the existence of genes possibly
 RT involved in chloroplast division."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
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 CC -----
 DR EMBL; AB001684; BAA57938.1; -.
 DR PIR; T07290; T07290.
 KW Photosystem I; Photosynthesis; Chloroplast.
 SQ SEQUENCE 31 AA; 3310 MW; 184858F3D8BD6873 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALA 5
 ||||
 Db 14 LALA 17

RESULT 18

PSAM_SYNY3

ID PSAM_SYNY3 STANDARD; PRT; 31 AA.
 AC P72986;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM OR SMR0005.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
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 CC -----
 DR EMBL; D90902; BAA17005.1; -.
 DR PIR; S74965; S74965.
 KW Photosystem I; Photosynthesis; Complete proteome.
 SQ SEQUENCE 31 AA; 3380 MW; 07E0E7E8CB2720F0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
 ||||
 Db 9 LAAL 12

RESULT 19

PSBZ_EUGST

ID PSBZ_EUGST STANDARD; PRT; 32 AA.
 AC Q8SL89;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Photosystem II reaction center Z protein (Fragment).
 GN PSBZ OR YCF9.
 OS Euglena stellata.
 OG Chloroplast.
 OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
 OX NCBI_TaxID=38278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21851312; PubMed=11861918;
 RA Sheveleva E.V., Giordani N.V., Hallick R.B.;
 RT "Identification and comparative analysis of the chloroplast alpha-
 RT subunit gene of DNA-dependent RNA polymerase from seven Euglena
 RT species.";
 RL Nucleic Acids Res. 30:1247-1254(2002).
 CC -!- FUNCTION: Controls the interaction of photosystem II (PSII) cores
 CC with the light-harvesting antenna (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 CC with the photosystem II complex (By similarity).
 CC -!- SIMILARITY: Belongs to the psbZ family.
 CC -----
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CC -----

DR EMBL; AY047486; AAL83365.1; -.
DR HAMAP; MF_00644; -; 1.
KW Photosynthesis; Photosystem II; Reaction center; Thylakoid;
KW Transmembrane; Chloroplast.
FT NON_TER 1 1
FT TRANSMEM 11 31 POTENTIAL.
SQ SEQUENCE 32 AA; 3566 MW; 9414D7D307878309 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LNSY 29
|||
Db 27 LNSY 30

RESULT 20

PBAN_LYMDI

ID PBAN_LYMDI STANDARD; PRT; 33 AA.
AC P43511;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Pheromone biosynthesis activating neuropeptide (LYD-PBAN).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Suboesophageal ganglion;
RX MEDLINE=95072631; PubMed=7981730;
RA Masler E.P., Raina A.K., Wagner R.M., Kochansky J.P.;
RT "Isolation and identification of a pheromonotropic neuropeptide from
RT the brain-suboesophageal ganglion complex of Lymantria dispar: a new
RT member of the PBAN family.";
RL Insect Biochem. Mol. Biol. 24:829-836(1994).
CC -!- FUNCTION: INVOLVED IN THE CONTROL OF PHEROMONE PRODUCTION IN
CC FEMALE GYPSY MOTH.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Hormone; Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 33 33 AMIDATION.
SQ SEQUENCE 33 AA; 3884 MW; E4CB1B8AFD3FEFC2 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LADD 7

Db ||||
 1 LADD 4

RESULT 21

YC12_MARPO

ID YC12_MARPO STANDARD; PRT; 33 AA.

AC P31560;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 3.4 kDa protein ycf12 (ORF 33).

GN YCF12.

OS Marchantia polymorpha (Liverwort).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;

OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;

OC Marchantiaceae; Marchantia.

OX NCBI_TaxID=3197;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89068687; PubMed=3199436;

RA Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,

RA Ozeki H., Ohyama K.;

RT "Structure and organization of Marchantia polymorpha chloroplast

RT genome. III. Gene organization of the large single copy region from

RT rbcL to trnI(CAU).";

RL J. Mol. Biol. 203:333-351(1988).

RN [2]

RP SEQUENCE FROM N.A.

RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,

RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,

RA Ozeki H.;

RT "Chloroplast gene organization deduced from complete sequence of

RT liverwort Marchantia polymorpha chloroplast DNA.";

RL Nature 322:572-574(1986).

CC -!- SIMILARITY: BELONGS TO THE YCF12 FAMILY.

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CC -----

DR EMBL; X04465; CAA28069.1; -.

DR PIR; S01581; A05010.

KW Chloroplast; Hypothetical protein.

SQ SEQUENCE 33 AA; 3386 MW; C88B5B778FF1C50D CRC64;

Query Match 10.3%; Score 4; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19

||||

RESULT 22

PETG_CYACA

ID PETG_CYACA STANDARD; PRT; 35 AA.
AC Q9TLQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit V (Cytochrome b6f complex subunit
DE petG).
GN PETG.
OS Cyanidium caldarium.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
RT genome.";
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: The cytochrome b6-f complex functions in the linear
CC cross-membrane transport of electrons between photosystem II and
CC I, as well as in cyclic electron flow around photosystem I. PetG
CC is required for either the stability or assembly of the cytochrome
CC b6-f complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
CC -!- SIMILARITY: Belongs to the petG family.
CC -----
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CC -----
DR EMBL; AF022186; AAF12884.1; -.
DR HAMAP; MF_00432; -; 1.
DR InterPro; IPR003683; Cytochrmb6/f_5.
DR Pfam; PF02529; PetG; 1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.
FT DOMAIN 1 4 LUMENAL (POTENTIAL).
FT TRANSMEM 5 25 POTENTIAL.
FT DOMAIN 26 35 STROMAL (POTENTIAL).
SQ SEQUENCE 35 AA; 3803 MW; B03C27094A1B74F3 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
||||
Db 21 LLAA 24

RESULT 23

PYY_RAJRH

ID PYY_RAJRH STANDARD; PRT; 36 AA.
AC P29206;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peptide YY-like (PYY).
OS Raja rhina (Skate).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualia; Pristiorajia; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=30478;
RN [1]
RP SEQUENCE.
RX MEDLINE=91296574; PubMed=2067973;
RA Conlon J.M., Bjerning C., Moon T.W., Youson J.H., Thim L.;
RT "Neuropeptide Y-related peptides from the pancreas of a teleostean
RT (eel), holostean (bowfin) and elasmobranch (skate) fish.";
RL Peptides 12:221-226(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NPY family.
DR HSSP; P01303; 1RON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation.
FT MOD_RES 36 36 AMIDATION.
SQ SEQUENCE 36 AA; 4251 MW; 07A7D9DC196660B6 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAA 9
||||
Db 10 DDAA 13

RESULT 24

DIU1_TENMO

ID DIU1_TENMO STANDARD; PRT; 37 AA.
AC P56618;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diuretic hormone I (DH I) (Diuretic peptide I) (DP I) (DH(37)).
OS Tenebrio molitor (Yellow mealworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=96109258; PubMed=8618894;
 RA Furuya K., Schegg K.M., Wang H., King D.S., Schooley D.A.;
 RT "Isolation and identification of a diuretic hormone from the mealworm
 RT Tenebrio molitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:12323-12327(1995).
 CC -!- FUNCTION: Increases cyclic AMP production in Malpighian tubules.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UROSENSIN I FAMILY OF PEPTIDES.
 DR PIR; A58607; A57127.
 DR InterPro; IPR000187; corticoliberin.
 DR Pfam; PF00473; CRF; 1.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 KW Hormone.
 SQ SEQUENCE 37 AA; 4371 MW; 519EC232D3473A85 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERAR 15
 ||||
 Db 20 ERAR 23

RESULT 25

RK36_NEPOL

ID RK36_NEPOL STANDARD; PRT; 37 AA.
 AC Q9TL26;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chloroplast 50S ribosomal protein L36.
 GN RPL36.
 OS Nephroselmis olivacea.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
 OC Chlorodendrales; Chlorodendraceae; Nephroselmis.
 OX NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIES-484;
 RX MEDLINE=99398694; PubMed=10468594;
 RA Turmel M., Otis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
 RT olivacea: insights into the architecture of ancestral chloroplast
 RT genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 CC -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----
DR EMBL; AF137379; AAD54790.1; -.
DR HSSP; P80256; 1DFE.
DR HAMAP; MF_00251; -; 1.
DR InterPro; IPR000473; Ribosomal_L36.
DR Pfam; PF00444; Ribosomal_L36; 1.
DR ProDom; PD002101; Ribosomal_L36; 1.
DR TIGRFAMS; TIGR01022; rpmJ_bact; 1.
DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein; Chloroplast.
SQ SEQUENCE 37 AA; 4429 MW; BC68BD516BF7FB37 CRC64;

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Query Match          10.3%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      32 KLLV 35
        ||||
Db      22 KLLV 25

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RESULT 26

CPRP_CANPG

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ID CPRP_CANPG STANDARD; PRT; 38 AA.
AC P81033;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CHH precursor related peptide (CPRP).
OS Cancer pagurus (Rock crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Cancroidea; Cancridae; Cancer.
OX NCBI_TaxID=6755;
RN [1]
RP SEQUENCE.
RC TISSUE=Sinus gland;
RX MEDLINE=99025664; PubMed=9809792;
RA Chung J.S., Wilkinson M.C., Webster S.G.;
RT "Amino acid sequences of both isoforms of crustacean hyperglycemic
RT hormone (CHH) and corresponding precursor-related peptide in Cancer
RT pagurus.";
RL Regul. Pept. 77:17-24(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN
CC THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE IT IS
CC STORED AND RELEASED.
DR InterPro; IPR005558; Crust_neuro_H.
DR Pfam; PF03858; Crust_neuro_H; 1.

```

KW Neuropeptide; Hormone.

SQ SEQUENCE 38 AA; 3969 MW; C979C87EE31ABB90 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RLLA 18

||||

Db 11 RLLA 14

RESULT 27

GVPC_SPICC

ID GVPC_SPICC STANDARD; PRT; 39 AA.

AC P81000;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gas vesicle protein C (Fragment).

GN GVPC.

OS Spirulina sp. (strain CCAP 1475/10).

OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.

OX NCBI_TaxID=69016;

RN [1]

RP SEQUENCE.

RX MEDLINE=92407497; PubMed=1527496;

RA Griffiths A.E., Walsby A.E., Hayes P.K.;

RT "The homologues of gas vesicle proteins.";

RL J. Gen. Microbiol. 138:1243-1250(1992).

CC -!- FUNCTION: May confer stability to the gas vesicle membranes. Gas
CC vesicles are small, hollow, gas filled protein structures that are
CC found in several microbial planktonic microorganisms. They allow
CC the positioning of the organism at the favorable depth for growth.

CC -!- SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
CC VESICLE MEMBRANE.

CC -!- SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE C FAMILY.

DR InterPro; IPR002003; Gas_vesicle_C.

DR PROSITE; PS00235; GAS_VESICLE_C; PARTIAL.

KW Gas vesicle.

FT NON_TER 1 1

FT NON_TER 39 39

SQ SEQUENCE 39 AA; 4487 MW; D9980C1C0CF459E7 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LERR 23

||||

Db 11 LERR 14

RESULT 28

NPF_MONEX

ID NPF_MONEX STANDARD; PRT; 39 AA.

AC P41967;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuropeptide F (NPF).
 OS *Moniezia expansa* (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Anoplocephalidae; *Moniezia*.
 OX NCBI_TaxID=28841;
 RN [1]
 RP SEQUENCE.
 RA Maule A.G., Shaw C., Halton D.W., Thim L., Johnston C.F.,
 RA Fairweather I., Buchanan K.D.;
 RT "Neuropeptide F: a novel parasitic flatworm regulatory peptide from
 RT *Moniezia expansa* (Cestoda: Cyclophyllidea).";
 RL Parasitology 102:309-316(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93096525; PubMed=1461689;
 RA Maule A.G., Shaw C., Halton D.W., Brennan G.P., Johnston C.F.,
 RA Moore S.;
 RT "Neuropeptide F (*Moniezia expansa*): localization and characterization
 RT using specific antisera.";
 RL Parasitology 105:505-512(1992).
 CC -!- FUNCTION: MAY HAVE AN IMPORTANT PHYSIOLOGICAL ROLE IN
 CC NEUROREGULATION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NPY family.
 DR PDB; 1K8V; 12-JUN-02.
 DR InterPro; IPR001955; Pancreatic_hormn.
 DR Pfam; PF00159; hormone3; 1.
 DR SMART; SM00309; PAH; 1.
 DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
 KW Neuropeptide; Amidation; 3D-structure.
 FT MOD_RES 39 39 AMIDATION.
 SQ SEQUENCE 39 AA; 4594 MW; 2D61A76927DEA732 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LVLD 37
 ||||
 Db 12 LVLD 15

RESULT 29

PHRI_BACSU

ID PHRI_BACSU STANDARD; PRT; 39 AA.
 AC 031492;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphatase rapI inhibitor (Phosphatase regulator I).
 GN PHRI.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."
 RL Nature 390:249-256(1997).
 CC -!- FUNCTION: Inhibitor of the activity of phosphatase rapI.
 CC -!- SIMILARITY: BELONGS TO THE PHR FAMILY.
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 CC -----
 DR EMBL; Z99106; CAB12309.1; -.
 DR PIR; E69677; E69677.
 DR SubtiList; BG12645; phrI.
 KW Complete proteome.
 SQ SEQUENCE 39 AA; 4232 MW; 5C716F587894B2DA CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
||||
Db 7 LLAA 10

RESULT 30

THIO_CLOSG

ID THIO_CLOSG STANDARD; PRT; 40 AA.
AC P81108;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thioredoxin (TRX) (Fragment).
GN TRXA.
OS Clostridium sporogenes.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1509;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 633;
RX MEDLINE=98195737; PubMed=9534247;
RA Harms C., Meyer M.A., Andreesen J.R.;
RT "Fast purification of thioredoxin reductases and of thioredoxins with
RT an unusual redox-active centre from anaerobic, amino-acid-utilizing
RT bacteria.";
RL Microbiology 144:793-800(1998).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
DR InterPro; IPR006662; Thioired.
DR InterPro; IPR006663; Thioredox_dom2.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center; Electron transport.
FT DISULFID 29 32 REDOX-ACTIVE (BY SIMILARITY).
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4525 MW; C7BE3C913E3E2909 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LVLD 37
||||
Db 2 LVLD 5

RESULT 31

UC11_MAIZE

ID UC11_MAIZE STANDARD; PRT; 40 AA.
AC P80617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 207)
DE (Fragments).

OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.2, ITS MW IS: 27.1 kDa.
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. HSP26 FAMILY.
 CC -!- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.
 DR Maize-2DPAGE; P80617; COLEOPTILE.
 DR MaizeDB; 123940; -.
 FT NON_TER 1 1
 FT NON_CONS 13 14
 FT NON_CONS 26 27
 FT NON_CONS 35 36
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4475 MW; 2ACD4BF8F4908277 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
 ||||
 Db 18 LLAA 21

RESULT 32

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
 AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved Mycobacterium smegmatis.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and

CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLA 3
 |||
 Db 20 SLA 22

RESULT 33

MAAI_RAT
 ID MAAI_RAT STANDARD; PRT; 28 AA.
 AC P57113;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Maleylacetoacetate isomerase (EC 5.2.1.2) (MAAI) (Glutathione S-
 DE transferase zeta 1) (EC 2.5.1.18) (GSTZ1-1) (Fragment).
 GN GSTZ1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=Fischer 344; TISSUE=Liver;
 RX MEDLINE=98198370; PubMed=9531472;
 RA Tong Z., Board P.G., Anders M.W.;
 RT "Glutathione transferase zeta catalyses the oxygenation of the
 RT carcinogen dichloroacetic acid to glyoxylic acid."
 RL Biochem. J. 331:371-374(1998).
 CC -!- FUNCTION: PROBABLE BIFUNCTIONAL ENZYME SHOWING MINIMAL
 CC GLUTATHIONE-CONJUGATING ACTIVITY WITH ETHACRYNIC ACID AND 7-
 CC CHLORO-4-NITROBENZ-2-OXA-1, 3-DIAZOLE AND MALEYLACETOACETATE
 CC ISOMERASE ACTIVITY. HAS ALSO LOW GLUTATHIONE PEROXIDASE ACTIVITY
 CC WITH T-BUTYL AND CUMENE HYDROPEROXIDES (BY SIMILARITY). IS ABLE TO
 CC CATALYZE THE GLUTATHIONE DEPENDENT OXYGENATION OF DICHLOROACETIC
 CC ACID TO GLYOXYLIC ACID.
 CC -!- CATALYTIC ACTIVITY: 4-maleylacetoacetate = 4-fumarylacetoacetate.
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -!- COFACTOR: THE MAAI ACTIVITY REQUIRES GLUTATHIONE (BY SIMILARITY).
 CC -!- PATHWAY: Phenylalanine catabolism; fifth step.
 CC -!- PATHWAY: Tyrosine catabolism; fourth step.
 CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ZETA FAMILY.
 KW Isomerase; Transferase; Multifunctional enzyme;
 KW Phenylalanine catabolism; Tyrosine catabolism.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2943 MW; 1070608C44491C25 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ALE 21
 |||
 Db 11 ALE 13

RESULT 34

OBP1_HYSCR

ID OBP1_HYSCR STANDARD; PRT; 28 AA.
 AC P81647;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Odorant-binding protein I (OBP I) (Olfactory mucosa pyrazine-binding
 DE protein I) (Fragment).
 OS Hystrix cristata (Crested porcupine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hystricidae; Hystrix.
 OX NCBI_TaxID=10137;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Nasal mucosa;
 RX MEDLINE=97370581; PubMed=9226887;
 RA Ganni M., Garibotti M., Scaloni A., Pucci P., Pelosi P.;
 RT "Microheterogeneity of odorant-binding proteins in the porcupine
 RT revealed by N-terminal sequencing and mass spectrometry."
 RL Comp. Biochem. Physiol. 117B:287-291(1997).
 RN [2]
 RP CHARACTERIZATION.
 RC TISSUE=Nasal mucosa;
 RX MEDLINE=93373535; PubMed=8365121;
 RA Felicioli A., Ganni M., Garibotti M., Pelosi P.;
 RT "Multiple types and forms of odorant-binding proteins in the Old-World
 RT porcupine Hystrix cristata."
 RL Comp. Biochem. Physiol. 105B:775-784(1993).
 CC -!- FUNCTION: This soluble protein may play a specific role in odor
 CC discrimination and perception.
 CC -!- SUBCELLULAR LOCATION: Secreted; Extracellular.
 CC -!- TISSUE SPECIFICITY: Nasal mucosa.
 CC -!- SIMILARITY: Belongs to the lipocalin family.
 DR HSSP; Q95182; 1EW3.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 KW Olfaction; Transport; Lipocalin.
 FT NON_TER 28 28

SQ SEQUENCE 28 AA; 3240 MW; D12E8CAC87E38AB3 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLA 18
|||
Db 21 LLA 23

RESULT 35

ORND_PLAOR

ID ORND_PLAOR STANDARD; PRT; 28 AA.
AC P25513;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornatin D (Fragment).
OS Placobdella ornata (Turtle leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Placobdella.
OX NCBI_TaxID=6415;
RN [1]
RP SEQUENCE.
RX MEDLINE=92111479; PubMed=1765068;
RA Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
RT "Ornatins: potent glycoprotein IIB-IIIA antagonists and platelet
RT aggregation inhibitors from the leech Placobdella ornata.";
RL Eur. J. Biochem. 202:1073-1082(1991).
CC -!- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET
CC RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY PREVENT
CC BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
CC INGESTED BLOOD.
CC -!- SIMILARITY: BELONGS TO THE ORNATIN FAMILY.
DR InterPro; IPR002463; Ornatin.
DR Pfam; PF02088; Ornatin; 1.
KW Blood coagulation; Platelet; Cell adhesion.
FT NON TER 28 28
SQ SEQUENCE 28 AA; 3361 MW; CFC38951F91337C2 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRE 12
|||
Db 16 FRE 18

RESULT 36

SMS2_ORENI

ID SMS2_ORENI STANDARD; PRT; 28 AA.
AC P81029;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin II precursor [Contains: [Tyr21,Gly24]somatostatin-28;
DE [Tyr7,Gly10]somatostatin-14] (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE.
RX MEDLINE=95384941; PubMed=7656183;
RA Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.;
RT "Characterization of the pancreatic hormones from the Brockmann body
RT of the tilapia: implications for islet xenograft studies.";
RL Comp. Biochem. Physiol. 111C:33-44(1995).
CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Cleavage on pair of basic residues; Hormone; Multigene family.
FT NON_TER 1 1
FT PEPTIDE 1 28 [TYR21,GLY24]SOMATOSTATIN-28.
FT PEPTIDE 15 28 [TYR7,GLY10]SOMATOSTATIN-14.
FT DISULFID 17 28
SQ SEQUENCE 28 AA; 3155 MW; 47C049F4866EF4AC CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RER 13
|||
Db 11 RER 13

RESULT 37

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
AC P48142; P01285;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RT and stomach of the alligator.";
RL Peptides 14:573-579(1993).

CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNS 28
 |||
 Db 23 LNS 25

RESULT 38

VIP_DIDMA

ID VIP_DIDMA STANDARD; PRT; 28 AA.
 AC P39089;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92179271; PubMed=1542675;
 RA Eng J., Yu J.-H., Rattan S., Yalow R.S.;
 RT "Isolation and amino acid sequences of opossum vasoactive intestinal
 RT polypeptide and cholecystokinin octapeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1809-1811(1992).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A38232; A38232.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3318 MW; F01188A0A72F76D9 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLL 17
|||
Db 12 RLL 14

RESULT 39

VIP_RANRI

ID VIP_RANRI STANDARD; PRT; 28 AA.
AC P81016;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RX MEDLINE=95309202; PubMed=7540547;
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
RT "Frog vasoactive intestinal polypeptide and galanin: primary
RT structures and effects on pituitary adenylate cyclase."
RL Endocrinology 136:3079-3086(1995).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNS 28
|||
Db 23 LNS 25

RESULT 40

VIP_SCYCA

ID VIP_SCYCA STANDARD; PRT; 28 AA.
AC P09685;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87299819; PubMed=2441759;
 RA Dimaline R., Young J., Thwaites D.T., Lee C.M., Shuttleworth T.J.,
 RA Thorndyke M.C.;
 RT "A novel vasoactive intestinal peptide (VIP) from elasmobranch
 RT intestine has full affinity for mammalian pancreatic VIP receptors.";
 RL Biochim. Biophys. Acta 930:97-100(1987).
 RN [2]
 RP SEQUENCE.
 RA Dimaline R., Young J., Thwaites D.T., Lee C.M., Thorndyke M.C.;
 RT "Amino acid sequence of a biologically active vasoactive intestinal
 RT peptide from the elasmobranch Scyliorhinus canicula.";
 RL Ann. N.Y. Acad. Sci. 527:621-623(1988).
 RN [3]
 RP SEQUENCE OF 1-10.
 RX MEDLINE=86234323; PubMed=3715063;
 RA Dimaline R., Thorndyke M.C., Young J.;
 RT "Isolation and partial sequence of elasmobranch VIP.";
 RL Regul. Pept. 14:1-10(1986).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60303; A60303.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3270 MW; 9014389573F81F3B CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLA 18
 |||
 Db 26 LLA 28

Search completed: January 14, 2004, 10:35:42
 Job time : 8.43925 secs